

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:46:20 ; Search time 9.24545 Seconds
(without alignments)
187.325 Million cell updates/sec

Title: US-09-846-033B-185
Perfect score: 17
Sequence: 1 gctgggggc 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 565832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09846033/runat_11042005_185610_24081/app_query.fasta_1.796
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09846033 @CGN 1 1 107 @runat_11042005_185610_24081 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	8	2	PT0724
2	17	100.0	8	2	JS0315
3	17	100.0	8	2	JS0316
4	17	100.0	8	2	JS0317
5	17	100.0	8	2	JS0318
6	17	100.0	8	2	JS1570
7	17	100.0	9	2	A24244
8	17	100.0	9	2	PT0634
9	17	100.0	9	2	PT0562
10	17	100.0	9	2	A60522
11	17	100.0	10	2	B33995
12	17	100.0	10	2	S08997
13	17	100.0	10	2	A60421
14	17	100.0	10	2	S08998

15	17	100.0	10	2	A26381	hypertrehalosemic
16	17	100.0	10	2	JC1416	hypertrehalosemic
17	17	100.0	10	2	S09138	hypertrehalosemic
18	17	100.0	10	2	A31571	hypertrehalosemic/
19	17	100.0	10	2	PH1344	Ig heavy chain DJ
20	17	100.0	10	2	PH0923	T-cell receptor be
21	17	100.0	10	2	A40753	aldehyde ferredoxi
22	17	100.0	10	2	H37196	bradykinin-potent
23	17	100.0	10	2	F33932	Ig mu chain J regi
24	17	100.0	10	2	S53789	neuropeptide Pec-H
25	17	100.0	10	2	A59173	nuclease Bhi (EC 3
26	17	100.0	11	2	B49164	chromogranin-B - r
27	17	100.0	11	2	PT0249	Ig heavy chain CRD
28	17	100.0	11	2	PH1343	Ig heavy chain DJ
29	17	100.0	12	2	S26548	T-cell receptor be
30	17	100.0	12	2	S26553	T-cell receptor be
31	17	100.0	12	2	PH1324	Ig heavy chain DJ
32	17	100.0	12	2	PH1308	Ig heavy chain DJ
33	17	100.0	12	2	S43957	Ig mu chain V regi
34	17	100.0	12	2	B49033	T-cell receptor de
35	17	100.0	13	1	MTCMAD	melanotropin alpha
36	17	100.0	13	1	MTHOAD	melanotropin alpha
37	17	100.0	13	2	PT0293	Ig heavy chain CRD
38	17	100.0	13	2	S57567	T-cell receptor V-
39	17	100.0	13	2	PH0928	T-cell receptor be
40	17	100.0	13	2	I51905	collecting duct wa
41	17	100.0	13	2	S66558	serine proteinase
42	17	100.0	14	2	S03530	Ig heavy chain J r
43	17	100.0	14	2	PT0223	Ig heavy chain CDR
44	17	100.0	14	2	PH1348	Ig heavy chain DJ
45	17	100.0	14	2	PH1356	Ig heavy chain DJ

ALIGNMENTS

RESULT 1

PT0724
T-cell receptor beta chain V-D-J region (140-2C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0724; PT0555
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0724
A:Status: translation not shown
A:Status: translation not shown
A:Molecule type: DNA
A:Molecule type: 1-8 <FEE>
A:Experimental source: newborn thymus, strain BALB/c (clone 140-2C)
A:Accession: PT0555
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c (clone 126-1AL)
C:Keywords: T-cell receptor

Alignment Scores:	2.4e+07	Length:	8
Pred. No.:	17.00	Matches:	2
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	2		

US-09-846-033B-185 (1-9) x PT0724 (1-8)

QY 3 TGGGGG 8

Db 7 TrpGly 8

RESULT 2

JS0315

leucokinin V - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0315
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19987
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Alignment Scores:
Pred. No.: 2.4e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-185 (1-9) x JS0315 (1-8)

Qy 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 3
JS0316
leucokinin VI - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0316
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0316
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19988
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Alignment Scores:
Pred. No.: 2.4e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-185 (1-9) x JS0316 (1-8)

Qy 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 4
JS0317
leucokinin VII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0317
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
A;Reference number: JS0317

A;Accession: JS0317
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19989
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Alignment Scores:
Pred. No.: 2.4e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-185 (1-9) x JS0317 (1-8)

Qy 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 5
JS0318
leucokinin VIII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0318
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
A;Reference number: JS0317
A;Accession: JS0318
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19990
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Alignment Scores:
Pred. No.: 2.4e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-185 (1-9) x JS0318 (1-8)

Qy 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 6
A31570
angiotensin-converting enzyme inhibitor - yellowfin tuna
C;Species: Thunnus albacares (yellowfin tuna)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31570
R;Kohama, Y.; Mateumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
Biochem. Biophys. Res. Commun. 155, 332-337, 1988
A;Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A;Reference number: A31570; MUID:88326322; PMID:3415688
A;Accession: A31570
A;Molecule type: protein
A;Residues: 1-8 <KOH>
A;Cross-references: UNIPROT:P18691
A;Note: the source is designated as Neothunnus macropterus
C;Superfamily: unassigned animal peptides
C;Keywords: angiotensin-converting enzyme inhibitor

Alignment Scores:

Pred. No.: 2.4e+07
Score: 17.00
Length: 8
Matches: 2
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 0

US-09-846-033B-185 (1-9) x A31570 (1-8)

QY 3 TGGGGG 8
Db 6 TrpGly 7

RESULT 7

A24244
adipokinetin hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helicoverpa zea
A:Reference number: A24244; PMID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAP>
A:Cross-references: UNIPROT:P08901
C:Superfamily: adipokinetin hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Alignment Scores:

Pred. No.: 2.14e+07
Score: 17.00
Length: 9
Matches: 2
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 0

US-09-846-033B-185 (1-9) x A24244 (1-9)

QY 3 TGGGGG 8
Db 8 TrpGly 9

RESULT 8

PT0634
T-cell receptor beta chain V-D-J region (121-2CL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0634
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; PMID:91277601; PMID:1711558
A:Accession: PT0634
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 2.14e+07
Score: 17.00
Length: 9
Matches: 2
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 0

US-09-846-033B-185 (1-9) x PT0634 (1-9)

QY 3 TGGGGG 8
Db 6 TrpGly 7

RESULT 9

PT0562
T-cell receptor beta chain V-D-J region (126-LAK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0562
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; PMID:91277601; PMID:1711558
A:Accession: PT0562
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 2.14e+07
Score: 17.00
Length: 9
Matches: 2
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 0

US-09-846-033B-185 (1-9) x PT0562 (1-9)

QY 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 10

A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: A60522
R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki, T.
Comp. Biochem. Physiol. B 95, 423-429, 1990
A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin, Diadema setosum.
A:Reference number: A60522; PMID:90227916; PMID:2158412
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <YOS>
A:Cross-references: UNIPROT:Q7M4D5
C:Superfamily: unassigned animal peptides
F:2-9/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 2.14e+07
Score: 17.00
Length: 9
Matches: 2
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 0

US-09-846-033B-185 (1-9) x A60522 (1-9)

QY 3 TGGGGG 8
Db 4 TrpGly 5

RESULT 11

B33995
hypotrehalosemic hormone - black horse fly
C:Species: Tabanus atratus (black horse fly)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C:Accession: B33995

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAP>
A;Cross-references: UNIPROT:P14596
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted
Alignment Scores:
Pred. No.: 4.59e+04 Length: 10
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-846-033B-185 (1-9) x B33995 (1-10)
QY 3 TGGGGG 8
Db 8 TrpGly 9
RESULT 12
S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S08997
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:P10939
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental
Alignment Scores:
Pred. No.: 4.59e+04 Length: 10
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-846-033B-185 (1-9) x S08997 (1-10)
QY 3 TGGGGG 8
Db 8 TrpGly 9
RESULT 13
A60421
hypertrehalosemic hormone - German cockroach
N;Alternate names: Bld-HrTH
C;Species: Blattella germanica (German cockroach)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60421; S09137
R;Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica
A;Reference number: A60421; MUID:91179584; PMID:2080017
A;Accession: A60421

A;Molecule type: protein
A;Residues: 1-10 <VEE>
A;Cross-references: UNIPROT:P10939
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental
Alignment Scores:
Pred. No.: 4.59e+04 Length: 10
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-846-033B-185 (1-9) x A60421 (1-10)
QY 3 TGGGGG 8
Db 8 TrpGly 9
RESULT 14
S08998
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S08998
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:P10939
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental
Alignment Scores:
Pred. No.: 4.59e+04 Length: 10
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-846-033B-185 (1-9) x S08998 (1-10)
QY 3 TGGGGG 8
Db 8 TrpGly 9
RESULT 15
A26381
hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A26381
R;Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardia

A:Reference number: A26381; MUID:87100208; PMID:3801028

A:Accession: A26381

A:Molecule type: protein

A:Residues: 1-10 <GAD>

A:Cross-references: UNIPROT:P10939

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Alignment Scores:

Pred. No.:	4.59e+04	Length:	10
Score:	17.00	Matches:	2
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-846-033b-185 (1-9) x A26381 (1-10)

QY 3 TGGGG 8

Db 8 TrpGly 9

Search completed: April 11, 2005, 19:11:47

Job time : 10.2455 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:45:50 ; Search time 42.8727 Seconds
(without alignments)
214.995 Million cell updates/sec

Title: US-09-846-033B-185
Perfect score: 17
Sequence: 1 gctg999gc 9

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/US09846033/runat.11042005.185609.24068/app.query.fasta_1.796
-DB=Uniprot -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEX=0 -LOOPEX1=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09846033 @CNC 1 1 427 @runat.11042005.185609.24068 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03.3*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	8	1 ACI_THUAL	P18691 thunnus alb
2	17	100.0	8	1 LCK1_LEUMA	P21140 leucophaea
3	17	100.0	8	1 LCK2_LEUMA	P21141 leucophaea
4	17	100.0	8	1 LCK3_LEUMA	P21142 leucophaea
5	17	100.0	8	1 LCK4_LEUMA	P21143 leucophaea
6	17	100.0	8	1 LCK5_LEUMA	P19987 leucophaea
7	17	100.0	8	1 LCK6_LEUMA	P19988 leucophaea
8	17	100.0	8	1 LCK7_LEUMA	P19990 leucophaea
9	17	100.0	8	1 LCK8_LEUMA	P26685 periplaneta
10	17	100.0	8	1 PK1_PERAM	P82686 periplaneta
11	17	100.0	8	1 PK2_PERAM	P82687 periplaneta
12	17	100.0	8	1 PK3_PERAM	P82688 periplaneta
13	17	100.0	8	1 PK4_PERAM	P82689 periplaneta
14	17	100.0	8	1 PK5_PERAM	P82929 bos taurus
15	17	100.0	8	1 RT34_BOVIN	Q70y57 fuerstia af
16	17	100.0	8	2 Q70Y57	

17	17	100.0	8	2 Q70Y84	Q70y84 plectranthu
18	17	100.0	8	2 Q6Z201	Q6z201 silene conl
19	17	100.0	8	2 Q6Z202	Q6z202 lychnis cor
20	17	100.0	9	1 AKH_HELZE	P67787 heliothis z
21	17	100.0	9	2 Q7M4D5	Q7m4d5 diadema set
22	17	100.0	9	2 Q94NA9	Q94na9 daubentonia
23	17	100.0	9	2 Q94NB0	Q94nb0 microcebus
24	17	100.0	9	2 Q94NB1	Q94nb1 microcebus
25	17	100.0	9	2 Q94NB2	Q94nb2 microcebus
26	17	100.0	9	2 Q94XE6	Q94xe6 tectocoris
27	17	100.0	9	2 Q85DB0	Q85db0 lepitemur s
28	17	100.0	9	2 Q85DB8	Q85db8 lepitemur e
29	17	100.0	9	2 Q6Z200	Q6z200 silene rotu
30	17	100.0	9	2 Q6VCX0	Q6vcx0 streptomyc
31	17	100.0	9	2 Q89491	Q89491 murine minu
32	17	100.0	10	1 BPP8_BOTIN	P30426 bothrops in
33	17	100.0	10	1 HTF1_ROMMI	P18110 romalea mic
34	17	100.0	10	1 HTF2_CARMO	P62542 carausius m
35	17	100.0	10	1 HTF2_EXTTI	P62543 extatosoma
36	17	100.0	10	1 HTF2_BLAGE	P84220 blattella g
37	17	100.0	10	1 HTF_GROPO	P84221 gromphadori
38	17	100.0	10	1 HTF_HELZE	P16353 heliothis z
39	17	100.0	10	1 HTF_LEUMA	P84219 leucophaea
40	17	100.0	10	1 HTF_NAUCI	P84218 nauphoeta c
41	17	100.0	10	1 HTF_TABAT	P14596 tabanus atr
42	17	100.0	10	1 LABA_JATMU	P13270 jatropa mu
43	17	100.0	10	2 Q7M530	Q7m530 pyrococcus
44	17	100.0	10	2 Q7M4X1	Q7m4x1 basidiobolu
45	17	100.0	10	2 Q7M465	Q7m465 platypleura

ALIGNMENTS

RESULT 1
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
RL FUNCTION: Inhibits angiotensin-converting enzyme.
DR PIR; A31570; A31570.
KW Direct protein sequencing; Metalloprotease inhibitor.
SQ SEQUENCE 8 AA; 953 MW; 6AA86373051F1B7 CRC64;

Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x ACI_THUAL (1-8)

QY 3 TGGGGG 8

Db 6 TrpGly 7

RESULT 2
LCK1_LEUMA
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protoderm (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 Glycine amide.
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;
Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x LCK1_LEUMA (1-8)
Qy 3 TGGGGG 8
Db 7 TrpGly 8
RESULT 3
LCK2_LEUMA
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protoderm (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 Glycine amide.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x LCK1_LEUMA (1-8)
Qy 3 TGGGGG 8
Db 7 TrpGly 8
RESULT 3
LCK2_LEUMA
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protoderm (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 Glycine amide.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x LCK2_LEUMA (1-8)
Qy 3 TGGGGG 8
Db 7 TrpGly 8

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x LCK2_LEUMA (1-8)
Qy 3 TGGGGG 8
Db 7 TrpGly 8
RESULT 4
LCK3_LEUMA
ID LCK3_LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protoderm (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 Glycine amide.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x LCK3_LEUMA (1-8)
Qy 3 TGGGGG 8
Db 7 TrpGly 8
RESULT 5
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protoderm (hindgut).
CC

CC -!- SUBCELLULAR LOCATION: Secreted.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 Glycine amide.
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Alignment Scores:
 Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x LCK4_LEUMA (1-8)

QY 3 TGGGGG 8
 Db |||||
 7 TrpGly 8

RESULT 6

LCK5_LEUMA
 ID LCK5_LEUMA STANDARD; PRT; 8 AA.
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberoidea; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE

TISSUE=Head;

RX MEDLINE=87052651; PubMed=2877794; DOI=10.1016/0742-8413(86)90077-0;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach prothodum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.

DR PIR; JS0315;
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 Glycine amide.
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C65B8 CRC64;

Alignment Scores:

Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x LCK5_LEUMA (1-8)

QY 3 TGGGGG 8
 Db |||||
 7 TrpGly 8

RESULT 7

LCK6_LEUMA
 ID LCK6_LEUMA STANDARD; PRT; 8 AA.
 AC P19988;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leucokinin VI (L-VI).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberoidea; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794; DOI=10.1016/0742-8413(86)90077-0;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach prothodum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0316; JS0316.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrolidone carboxylic acid. Pyrolidone carboxylic acid.
 FT MOD RES 1
 FT MOD RES 8
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Alignment Scores:

Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x LCK6_LEUMA (1-8)

QY 3 TGGGGG 8
 Db |||||
 7 TrpGly 8

RESULT 8

LCK7_LEUMA
 ID LCK7_LEUMA STANDARD; PRT; 8 AA.
 AC P19989;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberoidea; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE

TISSUE=Head;

RX MEDLINE=87052651; PubMed=2877794; DOI=10.1016/0742-8413(86)90077-0;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach prothodum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.

DR PIR; JS0317; JS0317.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 Glycine amide.
 SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9C6C76A CRC64;

Alignment Scores:

Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x LCK7_LEUMA (1-8)

QY 3 TGGGGG 8
 Db 7 TrpGly 8

RESULT 9
 LCK8_LEUMA
 ID_LCK8_LEUMA STANDARD; PRT; 8 AA.
 AC P19990;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach proctodeum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0318;
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 8 Glycine amide.
 SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Alignment Scores:
 Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x LCK8_LEUMA (1-8)

QY 3 TGGGGG 8
 Db 7 TrpGly 8

RESULT 10
 PK1_PERAM
 ID_PK1_PERAM STANDARD; PRT; 8 AA.
 AC P82685;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Kinin-1 (Pea-K-1).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
 RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).
 CC -!- MASS SPECTROMETRY: MW=949.26; METHOD=Electrospray; RANGE=1-8;

CC NOTE=Ref.1.
 CC -!- SIMILARITY: Belongs to the kinin family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 8 Glycine amide.
 SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Alignment Scores:
 Pred. No.: 1.28e+08 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-09-846-033B-185 (1-9) x PK1_PERAM (1-8)

QY 3 TGGGGG 8
 Db 7 TrpGly 8

RESULT 11
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 AC P82686;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Kinin-2 (Pea-K-2).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
 RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=855.04; METHOD=Electrospray; RANGE=1-8;

Alignment Scores:
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 Score: 17.00 Matches: 2
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 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x PK2_PERAM (1-8)

QY 3 TGGGGG 8
 Db 7 TrpGly 8

RESULT 12
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 ID_PK3_PERAM STANDARD; PRT; 8 AA.
 AC P82687;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

Score:	17.00	Matches:	2
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AC	P82689;		
DT	05-JUL-2004 (Rel. 44, Created)		
DT	05-JUL-2004 (Rel. 44, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Kinin-5 (Pea-K-5).		
OS	Periplaneta americana (American cockroach).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;		
OC	Blattidae; Periplaneta.		
OX	NCBI_TaxID=6978;		
RP	[1]		
RN	SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.		
RC	TISSUE=Corpora cardiaca;		
RA	MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;		
RX	Fredel R., Kellner R., Rapus J., Penzlin H., Gade G.;		
RT	"Isolation and structural elucidation of eight kinins from the		
RT	retrocerebral complex of the American cockroach, Periplaneta		
RT	americana.";		
RL	Regul. Pept. 71:199-205(1997).		
CC	FUNCTION: Mediates visceral muscle contractile activity (myotropic		
CC	activity).		
CC	SUBCELLULAR LOCATION: Secreted.		
CC	MASS SPECTROMETRY: MW=864.10; METHOD=Electrospray; RANGE=1-8;		
CC	NOTE=Ref.1.		
CC	SIMILARITY: Belongs to the kinin family.		
KW	Amidation; Direct protein sequencing; Neuropeptide.		
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AC	P82929;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).		
GN	Name=MRPS34;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RP	[1]		

RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123; DOI=10.1074/jbc.M100727200;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON_TER 1 1
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SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

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US-09-846-033B-185 (1-9) x RT34_BOVIN (1-8)

Qy 3 TGGGG 8
Db 2 TrpGly 3

Search completed: April 11, 2005, 19:09:48
Job time : 43.8727 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 19:09:59 ; Search time 35.6727 Seconds

(without alignments)
167.522 Million cell updates/sec

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Perfect score: 17

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Delop 6.0, Delext 7.0

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 2836020

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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1	17	100.0	8	8	US-08-424-550B-194	Sequence 194, Appl
2	17	100.0	8	9	US-09-113-696B-24	Sequence 24, Appl
3	17	100.0	8	9	US-09-947-925A-19	Sequence 19, Appl
4	17	100.0	8	9	US-09-947-925A-20	Sequence 20, Appl
5	17	100.0	8	9	US-09-875-519A-27	Sequence 27, Appl
6	17	100.0	8	9	US-09-791-378-397	Sequence 397, Appl
7	17	100.0	8	9	US-09-774-282-3	Sequence 3, Appl
8	17	100.0	8	9	US-09-984-245-143	Sequence 143, Appl
9	17	100.0	8	9	US-09-828-272A-3	Sequence 3, Appl
10	17	100.0	8	10	US-09-794-517-4	Sequence 4, Appl
11	17	100.0	8	10	US-09-986-480-361	Sequence 361, Appl
12	17	100.0	8	10	US-09-966-262-143	Sequence 143, Appl
13	17	100.0	8	10	US-09-880-748-2982	Sequence 2982, Appl
14	17	100.0	8	10	US-09-983-966-143	Sequence 143, Appl
15	17	100.0	8	10	US-09-794-529-4	Sequence 4, Appl
16	17	100.0	8	10	US-09-794-532-4	Sequence 4, Appl
17	17	100.0	8	10	US-09-865-548A-196	Sequence 196, Appl
18	17	100.0	8	10	US-09-972-656-62	Sequence 62, Appl
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20	17	100.0	8	11	US-09-922-227-7	Sequence 7, Appl
21	17	100.0	8	11	US-09-922-227-8	Sequence 8, Appl
22	17	100.0	8	11	US-09-791-377-397	Sequence 397, Appl
23	17	100.0	8	13	US-10-205-150-6	Sequence 6, Appl
24	17	100.0	8	14	US-10-101-482-1	Sequence 1, Appl
25	17	100.0	8	14	US-10-059-395-143	Sequence 143, Appl
26	17	100.0	8	14	US-10-094-699-72	Sequence 72, Appl
27	17	100.0	8	14	US-10-094-699-75	Sequence 75, Appl
28	17	100.0	8	14	US-10-033-741-73	Sequence 73, Appl
29	17	100.0	8	14	US-10-004-860-697	Sequence 697, Appl
30	17	100.0	8	14	US-10-094-401-182	Sequence 182, Appl
31	17	100.0	8	14	US-10-143-090-143	Sequence 143, Appl
32	17	100.0	8	14	US-10-023-282-697	Sequence 697, Appl
33	17	100.0	8	14	US-10-235-682-3	Sequence 3, Appl
34	17	100.0	8	14	US-10-193-768-52	Sequence 52, Appl
35	17	100.0	8	14	US-10-015-055-2	Sequence 2, Appl
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41	17	100.0	8	14	US-10-283-423-175	Sequence 175, Appl
42	17	100.0	8	14	US-10-283-423-176	Sequence 176, Appl
43	17	100.0	8	14	US-10-283-423-177	Sequence 177, Appl
44	17	100.0	8	14	US-10-283-423-178	Sequence 178, Appl
45	17	100.0	8	14	US-10-053-520-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-08-424-550B-194
; Sequence 194, Application US/08424550B
; Publication No. US2002011947A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK

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; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-194
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-424-550B-194 (1-8)

Qy 3 TGGGGG 8
Db 6 TrpGly 7

RESULT 2
US-09-113-696B-24
; Sequence 24, Application US/09113696B
; Patent No. US2002010134A1
; GENERAL INFORMATION:
; APPLICANT: Bhatnagar, Rajendra S.
; APPLICANT: Qian, Jing Jing
; APPLICANT: Gough, Craig
; TITLE OF INVENTION: PEPTIDE COMPOSITIONS MIMICKING TGF-BETA
; FILE REFERENCE: 6510-215CIP2
; CURRENT APPLICATION NUMBER: US/09/113,696B
; CURRENT FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/742,256
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: 08/431,954
; PRIOR FILING DATE: 1995-05-01
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TGF-beta mimic
; NAME/KEY: MOD_RES
; LOCATION: (7)...(7)
; OTHER INFORMATION: bala
; US-09-113-696B-24
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Alignment Scores:
Pred. No.: 8.09e+07 Length: 8
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Score: 17.00 Matches: 2
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US-09-846-033B-185 (1-9) x US-09-113-696B-24 (1-8)

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Db 2 TrpGly 3

RESULT 3
US-09-947-925A-19
; Sequence 19, Application US/09947925A
; Patent No. US20020055482A1
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
; TITLE OF INVENTION: Antigen Regulatory
; FILE REFERENCE: PB1087US3
; CURRENT APPLICATION NUMBER: US/09/947,925A
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/154,712
; PRIOR FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Consensus sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus sequence B2 from transcriptional dictionary
; OF Locker a
; OTHER INFORMATION: nd Buzard (1990).
; US-09-947-925A-19
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Score: 17.00 Matches: 2
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US-09-846-033B-185 (1-9) x US-09-947-925A-19 (1-8)

Qy 3 TGGGGG 8
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; Sequence 20, Application US/09947925A
; Patent No. US20020055482A1
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
; TITLE OF INVENTION: Antigen Regulatory
; FILE REFERENCE: PB1087US3
; CURRENT APPLICATION NUMBER: US/09/947,925A
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/154,712
; PRIOR FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; TYPE: PRT
; ORGANISM: Consensus sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus sequence B4 from transcriptional dictionary
; OTHER INFORMATION: of Locker a
; OTHER INFORMATION: nd Buzard (1990).
US-09-947-925A-20

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US-09-846-033B-185 (1-9) x US-09-947-925A-20 (1-8)

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Db       4 TrpGly 5

RESULT 5
US-09-875-519A-27
; Sequence 27, Application US/09875519A
; Patent No. US20020068059A1
; GENERAL INFORMATION:
; APPLICANT: Farries, Timothy C.
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
; FILE REFERENCE: 4-30443/A/IMU/PCT
; CURRENT APPLICATION NUMBER: US/09/875,519A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/GB97/00603
; PRIOR FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-519A-27

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QY      3 TGGGGG 8
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RESULT 6
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; Sequence 397, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0

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; ORGANISM: Homo sapiens
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QY      3 TGGGGG 8
Db       4 TrpGly 5

RESULT 7
US-09-774-282-3
; Sequence 3, Application US/09774282
; Publication No. US20020146374A1
; GENERAL INFORMATION:
; APPLICANT: LIPTON, JAMES M.
; TITLE OF INVENTION: A COMPOUND AND METHOD OF TREATMENT FOR FUNGAL PATHOLOGIES
; FILE REFERENCE: 54275, 8010, US00
; CURRENT APPLICATION NUMBER: US/09/774,282
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: n-term may or may not be acetylated
; FEATURE:
; OTHER INFORMATION: c-term may or may not be amidated
US-09-774-282-3

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches:      0
Query Match:     100.00%      Indels:         0
DB:              9          Gaps:         0

US-09-846-033B-185 (1-9) x US-09-774-282-3 (1-8)

QY      3 TGGGGG 8
Db       4 TrpGly 5

RESULT 8
US-09-984-245-143
; Sequence 143, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
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;; PRIOR FILING DATE: 1998-03-19
;; PRIOR APPLICATION NUMBER: US 60/041,277
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/042,344
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/041,276
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/041,281
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/048,094
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,350
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,188
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,135
;; PRIOR FILING DATE: 1997-05-30
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;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,187
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,099
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;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,186
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,069
;; PRIOR FILING DATE: 1997-05-30
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;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,096
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;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,160
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,351
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,154
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/054,804
;; PRIOR FILING DATE: 1997-08-05
;; PRIOR APPLICATION NUMBER: US 60/056,370
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: US 60/060,862
;; PRIOR FILING DATE: 1997-10-02
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 143
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-984-245-143

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Pred. No.: 17.00 Matches: 2
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 9

US-09-846-033B-185 (1-9) x US-09-984-245-143 (1-8)

Qy 3 TGGGGG 8
Db 3 Trpgly 4

RESULT 9

US-09-828-272A-3

;; Sequence 3, Application US/09828272A
;; Publication No. US20020183255A1
;; GENERAL INFORMATION:
;; APPLICANT: LIPTON, James M
;; APPLICANT: CATANIA, Anna P
;; TITLE OF INVENTION: USE OF KPV TRIPEPTIDE FOR DERMATOLOGICAL DISORDERS
;; FILE REFERENCE: 259/058
;; CURRENT APPLICATION NUMBER: US/09/828,272A
;; CURRENT FILING DATE: 2001-04-06
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 3
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Designed polypeptide with anti-inflammatory, anti-bacterial, anti
;; OTHER INFORMATION: -fungal and antipyrretic properties.
US-09-828-272A-3

Alignment Scores: 8.09e+07 Length: 8
Pred. No.: 17.00 Matches: 2
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 9

US-09-846-033B-185 (1-9) x US-09-828-272A-3 (1-8)

Qy 3 TGGGGG 8
Db 4 Trpgly 5

RESULT 10

US-09-794-517-4
;; Sequence 4, Application US/09794517
;; Publication No. US20030021794A1
;; GENERAL INFORMATION:
;; APPLICANT: Sloan-Kettering Institute for Cancer Research
;; ROTHMAN, James E.
;; HARTL, F. Ulrich
;; HOE, Mee H.
;; HOUGHTON, Alan
;; TAKECHI, Yoshizumi
;; MAYHEW, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and
;; Immunotherapies
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kenyon & Kenyon
;; STREET: One Broadway
;; CITY: New York
;; STATE: NY
;; COUNTRY: US
;; ZIP: 10004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/794,517
;; FILING DATE: 27-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/011,645
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 60/002,490
;; FILING DATE: August 18, 1995
;; APPLICATION NUMBER: PCT/US96/13363
;; FILING DATE: August 16, 1996
;; ATTORNEY/AGENT INFORMATION:

NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-517-4

Alignment Scores:
Pred. No.: 8.09e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-846-033B-185 (1-9) x US-09-794-517-4 (1-8)

Qy 3 TCGGGG 8
Db 2 TrpGly 3

RESULT 11
US-09-986-480-361
Sequence 361, Application US/09986480
Publication No. US20030027999A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/134,068
PRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 456
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 361
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-986-480-361

Alignment Scores:
Pred. No.: 8.09e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-846-033B-185 (1-9) x US-09-986-480-361 (1-8)

Qy 3 TCGGGG 8
Db 1 TrpGly 2

RESULT 12
US-09-966-262-143
Sequence 143, Application US/09966262
Publication No. US20030050461A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
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PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 143
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-262-143

Alignment Scores:
Pred. No.: 8.09e+07 Length: 8
Score: 17.00 Matches: 2

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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 10                           Gaps: 0

US-09-846-033B-185 (1-9) x US-09-966-262-143 (1-8)

Qy 3 TGGGGG 8
Db 3 Trpgly 4

RESULT 13
US-09-880-748-2982
; Sequence 2982, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2982
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2982

Alignment Scores:
Pred. No.: 8.09e+07      Length: 8
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Best Local Similarity: 100.00%    Mismatches: 0
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DB: 10                     Gaps: 0

US-09-846-033B-185 (1-9) x US-09-880-748-2982 (1-8)

Qy 3 TGGGGG 8
Db 2 Trpgly 3

RESULT 14
US-09-983-966-143
; Sequence 143, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21

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; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
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; PRIOR APPLICATION NUMBER: US 60/048,099
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; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-143

Alignment Scores:
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Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 10                     Gaps: 0

US-09-846-033B-185 (1-9) x US-09-983-966-143 (1-8)

Qy 3 TGGGGG 8
Db 3 Trpgly 4

RESULT 15
US-09-794-529-4
; Sequence 4, Application US/09794529
; Publication No. US20030082197A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; ROTHMAN, James E.
; HARTL, F. Ulrich
; HOE, Mee H.

```

HOUGHTON, Alan
TAKECHI, Yoshizumi
MAYHEW, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: One Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,529
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/011,645
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 60/002,479
FILING DATE: August 18, 1995
APPLICATION NUMBER: 60/002,490
FILING DATE: August 18, 1995
APPLICATION NUMBER: PCT/US96/13363
FILING DATE: August 16, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Delucia, Richard L.
REGISTRATION NUMBER: 28,839
REFERENCE/DOCKET NUMBER: 11746/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: <Unknown>
FEATURE:
OTHER INFORMATION: heat shock protein binding motif
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-794-529-4

Alignment Scores:
Pred. No.: 8.09e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-846-033B-185 (1-9) x US-09-794-529-4 (1-8)

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Db 2 TrpGly 3

Search completed: April 11, 2005, 19:55:30
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:49:31 ; Search time 10.5545 Seconds
(without alignments)
127.308 Million cell updates/sec

Title: US-09-846-033B-185
Perfect score: 17
Sequence: 1 gctgggggc 9

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Ygapop 10.0, Ygapext 0.5
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Delop 6.0, Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	100.0	8	1	Sequence 42, Appl
5	17	100.0	8	1	Sequence 3, Appl
6	17	100.0	8	1	Sequence 20, Appl
7	17	100.0	8	1	Sequence 21, Appl
8	17	100.0	8	1	Sequence 3, Appl
9	17	100.0	8	1	Sequence 10, Appl
10	17	100.0	8	1	Sequence 4, Appl
11	17	100.0	8	1	Sequence 7, Appl
12	17	100.0	8	1	Sequence 8, Appl
13	17	100.0	8	1	Sequence 2, Appl

13	17	100.0	8	1	US-08-525-654A-150
14	17	100.0	8	1	Sequence 31, Appl
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43	17	100.0	8	2	Sequence 22, Appl
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					Sequence 2, Appl
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					Sequence 74, Appl
					US-08-862-855-7
					Sequence 7, Appl
					US-08-862-855-8
					Sequence 8, Appl
					US-09-258-275-5
					Sequence 5, Appl
					US-09-203-231-64
					Sequence 64, Appl
					US-08-444-818-300
					Sequence 300, Appl
					US-08-444-818-301
					Sequence 301, Appl

ALIGNMENTS

RESULT 1
US-07-938-334C-22
; Sequence 22, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,334C
FILING DATE: 31-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5405940man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-938-334C-22

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-07-938-334C-22 (1-8)

Qy 3 TGGGGG 8
Db 4 TrpGly 5

RESULT 2
US-08-014-426-26
; Sequence 26, Application US/08014426
; Patent No. 5512435
; GENERAL INFORMATION:
; APPLICANT: Renschler, Markus F.
; APPLICANT: Levy, Ronald
; APPLICANT: Bhatt, Ramesh
; APPLICANT: Dower, William
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-204
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-014-426-26

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-014-426-26 (1-8)
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Qy 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 3
US-08-014-426-42
; Sequence 42, Application US/08014426
; Patent No. 5512435
; GENERAL INFORMATION:
; APPLICANT: Renschler, Markus F.
; APPLICANT: Levy, Ronald
; APPLICANT: Bhatt, Ramesh
; APPLICANT: Dower, William
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-204
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-014-426-42

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-014-426-42 (1-8)

Qy 3 TGGGGG 8
Db 2 TrpGly 3

RESULT 4
US-08-191-571-3
; Sequence 3, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
```

;; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marion Merrell Dow Inc.
;; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
;; CITY: Cincinnati
;; STATE: Ohio
;; COUNTRY: United States
;; ZIP: 45215-6300
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 03-FEB-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Boudreaux, William R
;; REGISTRATION NUMBER: 35,796
;; REFERENCE/DOCKET NUMBER: M01718
;; TELEPHONE: 513-948-6566
;; TELEFAX: 513-948-7961 or 4681
;; TELEX: 214320
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: circular
;; MOLECULE TYPE: peptide
US-08-191-571-3
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x US-08-191-571-3 (1-8)
QY 3 TGGGGG 8
Db 7 TrpGly 8
RESULT 5
US-08-191-571-20
; Sequence 20, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 03-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide

;; FILING DATE: 03-FEB-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Boudreaux, William R
;; REGISTRATION NUMBER: 35,796
;; REFERENCE/DOCKET NUMBER: M01718
;; TELEPHONE: 513-948-6566
;; TELEFAX: 513-948-7961 or 4681
;; TELEX: 214320
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: circular
;; MOLECULE TYPE: peptide
US-08-191-571-20
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x US-08-191-571-20 (1-8)
QY 3 TGGGGG 8
Db 3 TrpGly 4
RESULT 6
US-08-191-571-21
; Sequence 21, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 03-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide

FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa at location 4 is
; OTHER INFORMATION: glutamic acid in the D-configuration"
US-08-191-571-21

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-191-571-21 (1-8)

QY 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 7
US-08-424-567-3
; Sequence 3, Application US/08424567
; Patent No. 5569755
; GENERAL INFORMATION:
; APPLICANT: SCHWEINFEST, Clifford W.
; APPLICANT: PAPAS, Takis S.
; TITLE OF INVENTION: Colon Mucosa Gene Having Down-Regulated
; TITLE OF INVENTION: Expression In Colon Adenomas And Adenocarcinomas
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,567
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,045
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/181 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-424-567-3 (1-8)

QY 3 TGGGGG 8
Db 2 TrpGly 3

RESULT 8
US-08-002-466-10
; Sequence 10, Application US/08002466
; Patent No. 5580561
; GENERAL INFORMATION:
; APPLICANT: Cercek, Boris
; APPLICANT: Cercek, Lea
; TITLE OF INVENTION: Inhibition of Suppression of Immune
; TITLE OF INVENTION: Defense Caused by Peptides Active in the Structuredness of
; TITLE OF INVENTION: the Cytoplasmic Matrix (SCM) Assay
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,466
; FILING DATE: 19930108
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,686
; FILING DATE: 18-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/167/007
; FILING DATE: 03-MAR-1988
; PRIOR APPLICATION DATA: US 07/022,759
; APPLICATION NUMBER: 06-MAR-1987
; FILING DATE: 06-MAR-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 8941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-002-466-10

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-002-466-10 (1-8)

QY 3 TGGGGG 8
Db 2 TrpGly 3

RESULT 9
US-08-417-624-4
; Sequence 4, Application US/08417624
; Patent No. 5618685
; GENERAL INFORMATION:
; APPLICANT: Darke, Paul L.
; APPLICANT: Hall, Dawn L.
; TITLE OF INVENTION: ACTIVATION OF HERPES SIMPLEX VIRUS
; TITLE OF INVENTION: PROTEASE BY KOSMOTROPES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ms. Joanne M. Giesser
; STREET: 126 E. Lincoln Ave. P.O. Box 2000-0900
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,624
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesser, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19378
; TELEPHONE: (908) 594-3046
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-417-624-4

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033b-185 (1-9) x US-08-417-624-4 (1-8)
QY 3 TGGGGG 8
Db 7 TrpGly 8

RESULT 10
US-08-526-710-7
; Sequence 7, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,710
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-526-710-7

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033b-185 (1-9) x US-08-526-710-7 (1-8)
QY 3 TGGGGG 8
Db 4 TrpGly 5

RESULT 11
US-08-526-710-8
; Sequence 8, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,710
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-8
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x US-08-526-710-8 (1-8)
Qy 3 TGGGGG 8
Db 4 TrpGly 5
RESULT 12
US-08-482-880-2
; Sequence 2, Application US/08482880
; Patent No. 5736122
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.880
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5736122nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 1..5
; OTHER INFORMATION: /label= thioether
; OTHER INFORMATION: /note= "The sidechain sulfur atom of the cysteine
; OTHER INFORMATION: residue is covalently linked to the group [CH2CO],
; OTHER INFORMATION: which group forms an amide bond with the
US-08-482-880-2
Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x US-08-482-880-2 (1-8)
Qy 3 TGGGGG 8
Db 6 TrpGly 7
RESULT 13
US-08-525-654A-150
; Sequence 150, Application US/08525654A
; Patent No. 5736356
; GENERAL INFORMATION:
; APPLICANT: SANO, KOHICHIRO
; APPLICANT: KUMAZAWA, YOSHIYUKI
; APPLICANT: YASEUDA, HISASHI
; APPLICANT: SEGURO, KAISUYA
; APPLICANT: MOTOKI, MASAO
; TITLE OF INVENTION: TRANSGLUTAMINASE ORIGINATED FROM
; TITLE OF INVENTION: CRASSOSTREA GIGAS
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,654A
; FILING DATE: 28-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/8283
; FILING DATE: 28-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7/3876
; FILING DATE: 13-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-760-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-525-654A-150
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-525-654A-150 (1-8)

QY 3 TGGGGG 8
Db 4 TrpGly 5

RESULT 14

US-08-446-206B-31
; Sequence 31, Application US/08446206B
; Patent No. 5750647
; GENERAL INFORMATION:
; APPLICANT: Eyre, David R
; APPLICANT: Clemens, J Daniel
; TITLE OF INVENTION: Synthetic Peptide Analogs of NTX
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson & Kindness PLLC
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,206B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WRO18360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 682 8100
; TELEFAX: 206 224 0779
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; FEATURE:
; LOCATION: 1
; OTHER INFORMATION: Xaa is glutamine or pyrrolidone
; OTHER INFORMATION: carboxylic acid.
US-08-446-206B-31

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-446-206B-31 (1-8)

QY 3 TGGGGG 8
Db 5 TrpGly 6

RESULT 15

US-08-471-058-1

; Sequence 1, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-1

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x US-08-471-058-1 (1-8)

QY 3 TGGGGG 8
Db 2 TrpGly 3

Search completed: April 11, 2005, 19:14:00
Job time : 11.5545 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:41:45 ; Search time 50.7273 Seconds
(without alignments)
137.238 Million cell updates/sec

Title: US-09-846-033B-185
Perfect score: 17
Sequence: 1 gctgggggc 9

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=A_Geneseq -GFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09846033 @CN 1 1 475 @runat_11042005_185608_24062 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004as:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	8	1 AAP90275	Aap90275 Sequence
2	17	100.0	8	1 AAP90589	Aap90589 Synthetic
3	17	100.0	8	1 AAP91780	Aap91780 Synthetic
4	17	100.0	8	1 AAP90684	Aap90684 Synthetic
5	17	100.0	8	1 AAP90545	Aap90545 Synthetic
6	17	100.0	8	1 AAP91777	Aap91777 Synthetic
7	17	100.0	8	1 AAP91779	Aap91779 Synthetic
8	17	100.0	8	1 AAP91781	Aap91781 Synthetic
9	17	100.0	8	1 AAP91778	Aap91778 Synthetic
10	17	100.0	8	1 AAP91787	Aap91787 Synthetic

11	17	100.0	8	1 AAP91784	Aap91784 Synthetic
12	17	100.0	8	1 AAP91786	Aap91786 Synthetic
13	17	100.0	8	1 AAP91788	Aap91788 Synthetic
14	17	100.0	8	1 AAP91782	Aap91782 Synthetic
15	17	100.0	8	1 AAP90683	Aap90683 Synthetic
16	17	100.0	8	1 AAP91785	Aap91785 Synthetic
17	17	100.0	8	1 AAP91783	Aap91783 Synthetic
18	17	100.0	8	2 AAR11895	Aar11895 Lycium B
19	17	100.0	8	2 AAR22036	Aar22036 Cyclic pe
20	17	100.0	8	2 AAR27176	Aar27176 Sequence
21	17	100.0	8	2 AAR35816	Aar35816 Hepatitis
22	17	100.0	8	2 AAR35817	Aar35817 Hepatitis
23	17	100.0	8	2 AAR35843	Aar35843 Hepatitis
24	17	100.0	8	2 AAR35842	Aar35842 Hepatitis
25	17	100.0	8	2 AAR35818	Aar35818 Hepatitis
26	17	100.0	8	2 AAR35839	Aar35839 Hepatitis
27	17	100.0	8	2 AAR35840	Aar35840 Hepatitis
28	17	100.0	8	2 AAR35841	Aar35841 Hepatitis
29	17	100.0	8	2 AAR60434	Aar60434 Antiprol
30	17	100.0	8	2 AAR60450	Aar60450 Antiprol
31	17	100.0	8	2 AAR60268	Aar60268 Synthetic
32	17	100.0	8	2 AAR72125	Aar72125 Cell dama
33	17	100.0	8	2 AAR60569	Aar60569 Human ets
34	17	100.0	8	2 AAR67283	Aar67283 Hepatitis
35	17	100.0	8	2 AAR77203	Aar77203 Mouse ant
36	17	100.0	8	2 AAR93717	Aar93717 Cyclo(-Ty
37	17	100.0	8	2 AAR93716	Aar93716 Cyclo(-Le
38	17	100.0	8	2 AAR66786	Aar66786 Internal
39	17	100.0	8	2 AAR72653	Aar72653 Cladospor
40	17	100.0	8	2 AAR78641	Aar78641 Immunogen
41	17	100.0	8	2 AAR72989	Aar72989 H10D aml
42	17	100.0	8	2 AAR80502	Aar80502 Japanese
43	17	100.0	8	2 AAY16510	Aay16510 Betide se
44	17	100.0	8	2 AAR91214	Aar91214 Reverse c
45	17	100.0	8	2 AAW13418	Aaw13418 Brain hom

ALIGNMENTS

RESULT 1

AAP90275
ID AAP90275 standard; protein; 8 AA.

XX AC AAP90275;
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 14-MAR-1992 (first entry)

DE DE Sequence of peptide from Pacific yellow-finned tuna having Angiotensin I
XX DE converting enzyme (ACE) inhibitory activity.

KW Antihypertensive agent; Angiotensin I converting enzyme; inhibitor.

OS Thunnus albacares.

XX PN EP345778-A.

XX PD 13-DEC-1989.

XX PF 08-JUN-1989; 89EP-00110386.

XX PR 10-JUN-1988; 88JP-00143258.

XX PA (NIUS) NIPPON SUISAN KAISHA LTD.

XX PA (MOCH) MOCHIDA PHARM CO LTD.

XX PI Mimura T, Kohama Y, Satake M, Nagase Y;

XX DR WPI; 1989-365558/50.

XX PT New octa-peptide isolated from fish tissue - having Angiotensin I
PT converting enzyme inhibitory activity useful as an antihypertensive

PT agent.
 XX Claim 6; Page 7; 11pp; English.
 XX The peptide of the invention shows excellent ACE inhibitory activity and
 CC is useful as an antihypertensive agent, having low toxicity and good
 CC stability. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-
 CC OCT-2003 to standardise OS field)
 XX
 XX Sequence 8 AA;
 SQ

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP90275 (1-8)

Oy 3 TGGGGG 8
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 Db 6 TrpGly 7

RESULT 2
 AAP90689
 ID AAP90689 standard; peptide; 8 AA.
 XX
 AC AAP90689;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 01-FEB-1990 (first entry)
 XX
 XX Synthetic SCM-active cancer recognition peptide.
 DE
 XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
 KW
 XX Homo sapiens.
 OS
 XX WO8908118-A.
 PN
 XX 08-SEP-1989.
 PD
 XX 01-MAR-1989; 89WO-US000816.
 PF
 XX 02-MAR-1988; 88US-00163250.
 PR
 XX (CERC/) CERCEK B.
 PA
 XX Cercek B, Cercek L;
 PI
 XX WPI; 1989-278286/38.
 DR
 XX N-PSDB; AAN90939.
 DR
 XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
 PT antibodies used to provide sensitive assays for detecting malignancy.
 PT
 XX Claim 7; Table 2; 40pp; English.
 PS
 XX matrix (SCM) test; responding lymphocyte The peptide reacts with
 XX lymphocytes from donors with any type of malignancy. It can be used as a
 CC challenging agent in the SCM test which is used to distinguish
 CC lymphocytes isolated from mammals with cancer from those isolated from
 CC donors free of malignancy. It is one of a class of peptides which differ
 CC from each other by 'conservative' amino acid substitutions. Called
 CC Peptide II. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 XX Sequence 8 AA;
 SQ

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP90689 (1-8)

Oy 3 TGGGGG 8
 |||||
 Db 2 TrpGly 3

RESULT 3
 AAP91780
 ID AAP91780 standard; peptide; 8 AA.
 XX
 AC AAP91780;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 01-FEB-1990 (first entry)
 XX
 XX Synthetic SCM-active cancer recognition peptide.
 DE
 XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
 KW
 XX Homo sapiens.
 OS
 XX WO8908118-A.
 PN
 XX 08-SEP-1989.
 PD
 XX 01-MAR-1989; 89WO-US000816.
 PF
 XX 02-MAR-1988; 88US-00163250.
 PR
 XX (CERC/) CERCEK B.
 XX
 XX Cercek B, Cercek L;
 PI
 XX WPI; 1989-278286/38.
 DR
 XX N-PSDB; AAN90945.
 DR
 XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
 PT antibodies used to provide sensitive assays for detecting malignancy.
 PT
 XX Claim 6; Table 2; 40pp; English.
 PS
 XX matrix (SCM) test; responding lymphocyte The peptide reacts with
 XX lymphocytes from donors with any type of malignancy. It can be used as a
 CC challenging agent in the SCM test which is used to distinguish
 CC lymphocytes isolated from mammals with cancer from those isolated from
 CC donors free of malignancy. It is one of a group of peptides which differ
 CC from each other by 'conservative' amino acid substitutions. (Updated on
 CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 8 AA;
 SQ

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP91780 (1-8)

Oy 3 TGGGGG 8
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Db          2 TrpGly 3
RESULT 4
AAP90684
ID AAP90684 standard; peptide; 8 AA.
XX
AC AAP90684;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 01-FEB-1990 (first entry)
XX
DE Synthetic SCM-active cancer recognition peptide.
XX
XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
XX
XX Homo sapiens.
XX
XX WO8908118-A.
XX
XX 08-SEP-1989.
XX
XX 01-MAR-1989; 89WO-US000816.
XX
XX 02-MAR-1988; 88US-00163250.
XX
XX (CERC/) CERCEK B.
XX
XX Cercek B, Cercek L;
XX
XX WPI; 1989-278286/38.
XX
XX N-PSDB; AAN90941.
XX
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
XX antibodies used to provide sensitive assays for detecting malignancy.
XX
XX Claim 6; Table 2; 40pp; English.
XX
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
XX lymphocytes from donors with any type of malignancy. It can be used as a
XX challenging agent in the SCM test which is used to distinguish
XX lymphocytes isolated from mammals with cancer from those isolated from
XX donors free of malignancy. It is one of a group of peptides which differ
XX from each other by 'conservative' amino acid substitutions. (Updated on
XX 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 8 AA;
XX
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x AAP90684 (1-8)
QY 3 TGGGGG 8
DB 2 TrpGly 3
RESULT 5
AAP90545
ID AAP90545 standard; peptide; 8 AA.
XX
AC AAP90545;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 01-FEB-1990 (first entry)
XX
DE Synthetic SCM-active cancer recognition peptide.
XX
XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
XX
XX Homo sapiens.
XX
XX WO8908118-A.
XX
XX 08-SEP-1989.
XX
XX 01-MAR-1989; 89WO-US000816.
XX
XX 02-MAR-1988; 88US-00163250.
XX
XX (CERC/) CERCEK B.
XX
XX Cercek B, Cercek L;
XX
XX WPI; 1989-278286/38.
XX
XX N-PSDB; AAN90941.
XX
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
XX antibodies used to provide sensitive assays for detecting malignancy.
XX
XX Claim 6; Table 2; 40pp; English.
XX
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
XX lymphocytes from donors with any type of malignancy. It can be used as a
XX challenging agent in the SCM test which is used to distinguish
XX lymphocytes isolated from mammals with cancer from those isolated from
XX donors free of malignancy. It is one of a group of peptides which differ
XX from each other by 'conservative' amino acid substitutions. (Updated on
XX 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 8 AA;
XX
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x AAP90545 (1-8)
QY 3 TGGGGG 8
DB 2 TrpGly 3
RESULT 6
AAP91777
ID AAP91777 standard; peptide; 8 AA.
XX
AC AAP91777;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 01-FEB-1990 (first entry)
XX
DE Synthetic SCM-active cancer recognition peptide.
XX
XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
XX
XX Homo sapiens.
XX
XX WO8908118-A.
XX
XX 08-SEP-1989.
XX
XX 01-MAR-1989; 89WO-US000816.
XX
XX

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PR 02-MAR-1988; 88US-00163250.
XX (CERC/) CERCEK B.
XX Cercek B, Cercek L;
XX WPI; 1989-278286/38.
XX N-PSDB; AAN90943.
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
XX antibodies used to provide sensitive assays for detecting malignancy.
XX Claim 6; Table 2; 40pp; English.
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
XX lymphocytes from donors with any type of malignancy. It can be used as a
XX challenging agent in the SCM test which is used to distinguish
XX lymphocytes isolated from mammals with cancer from those isolated from
XX donors free of malignancy. It is one of a group of peptides which differ
XX from each other by 'conservative' amino acid substitutions. (Updated on
XX 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 8 AA;
XX Alignment Scores:
XX Pred. No.: 9.59e+07 Length: 8
XX Score: 17.00 Matches: 2
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 1 Gaps: 0
XX US-09-846-033B-185 (1-9) x AAP91777 (1-8)
XX QY 3 TGGGGG 8
XX DB 2 TrpGly 3
XX RESULT 7
XX AAP91779
XX ID AAP91779 standard; peptide; 8 AA.
XX AC AAP91779;
XX 25-MAR-2003 (revised)
XX 09-JAN-2003 (revised)
XX 01-FEB-1990 (first entry)
XX Synthetic SCM-active cancer recognition peptide.
XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
XX Homo sapiens.
XX WO8908118-A.
XX 08-SEP-1989.
XX 01-MAR-1989; 89WO-US000816.
XX 02-MAR-1988; 88US-00163250.
XX (CERC/) CERCEK B.
XX Cercek B, Cercek L;
XX WPI; 1989-278286/38.
XX N-PSDB; AAN90945.
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
XX antibodies used to provide sensitive assays for detecting malignancy.

PS Claim 6; Table 2; 40pp; English.
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
XX lymphocytes from donors with any type of malignancy. It can be used as a
XX challenging agent in the SCM test which is used to distinguish
XX lymphocytes isolated from mammals with cancer from those isolated from
XX donors free of malignancy. It is one of a group of peptides which differ
XX from each other by 'conservative' amino acid substitutions. (Updated on
XX 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 8 AA;
XX Alignment Scores:
XX Pred. No.: 9.59e+07 Length: 8
XX Score: 17.00 Matches: 2
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 1 Gaps: 0
XX US-09-846-033B-185 (1-9) x AAP91779 (1-8)
XX QY 3 TGGGGG 8
XX DB 2 TrpGly 3
XX RESULT 8
XX AAP91781
XX ID AAP91781 standard; peptide; 8 AA.
XX AC AAP91781;
XX 25-MAR-2003 (revised)
XX 09-JAN-2003 (revised)
XX 01-FEB-1990 (first entry)
XX Synthetic SCM-active cancer recognition peptide.
XX Cancer detection; malignancy detection; structuredness of cytoplasmic.
XX Homo sapiens.
XX WO8908118-A.
XX 08-SEP-1989.
XX 01-MAR-1989; 89WO-US000816.
XX 02-MAR-1988; 88US-00163250.
XX (CERC/) CERCEK B.
XX Cercek B, Cercek L;
XX WPI; 1989-278286/38.
XX N-PSDB; AAN90947.
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
XX antibodies used to provide sensitive assays for detecting malignancy.
XX Disclosure; Page 17; 40pp; English.
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
XX lymphocytes from donors with any type of malignancy. It can be used as a
XX challenging agent in the SCM test which is used to distinguish
XX lymphocytes isolated from mammals with cancer from those isolated from
XX donors free of malignancy. It is one of a group of peptides which differ
XX from each other by 'conservative' amino acid substitutions. It is called
XX Peptide III. (Updated on 09-JAN-2003 to add missing OS field.) (Updated
XX on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
XX PI field.)

SQ Sequence 8 AA;
 Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP91781 (1-8)

Qy 3 TGGGGG 8
 Db 3 TrpGly 4

RESULT 9

AAP91778
 ID AAP91778 standard; peptide; 8 AA.

XX AC AAP91778;

XX DT 25-MAR-2003 (revised)

XX DT 09-JAN-2003 (revised)

XX DT 01-FEB-1990 (first entry)

XX DE Synthetic SCM-active cancer recognition peptide.

XX KW Cancer detection; malignancy detection; structuredness of cytoplasmic.

XX OS Homo sapiens.

XX PN WO8908118-A.

XX PD 08-SEP-1989.

XX PF 01-MAR-1989; 89WO-US000816.

XX PR 02-MAR-1988; 88US-00163250.

XX PA (CERC/) CERCEK B.

XX PI Cercek B, Cercek L;

XX DR WPI; 1989-278286/38.

XX DR N-PSDB; AAN90944.

XX PT Synthetic SCM-active cancer recognition peptide(s) - DNA probes and

XX PT antibodies used to provide sensitive assays for detecting malignancy.

XX PS Claim 6; Table 2; 40pp; English.

XX CC matrix (SCM) test; responding lymphocyte The peptide reacts with
 CC lymphocytes from donors with any type of malignancy. It can be used as a
 CC challenging agent in the SCM test which is used to distinguish
 CC lymphocytes isolated from mammals with cancer from those isolated from
 CC donors free of malignancy. It is one of a group of peptides which differ
 CC from each other by 'conservative' amino acid substitutions. (Updated on
 CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP91778 (1-8)

Qy 3 TGGGGG 8
 Db 2 TrpGly 3

RESULT 10

AAP91787

ID AAP91787 standard; peptide; 8 AA.

XX AC AAP91787;

XX DT 25-MAR-2003 (revised)

XX DT 09-JAN-2003 (revised)

XX DT 01-FEB-1990 (first entry)

XX DE Synthetic SCM-active cancer recognition peptide.

XX KW Cancer detection; malignancy detection; structuredness of cytoplasmic.

XX OS Homo sapiens.

XX PN WO8908118-A.

XX PD 08-SEP-1989.

XX PF 01-MAR-1989; 89WO-US000816.

XX PR 02-MAR-1988; 88US-00163250.

XX PA (CERC/) CERCEK B.

XX PI Cercek B, Cercek L;

XX DR WPI; 1989-278286/38.

XX DR N-PSDB; AAN90953.

XX PT Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
 XX PT antibodies used to provide sensitive assays for detecting malignancy.

XX PS Disclosure; Page; 40pp; English.

XX CC matrix (SCM) test; responding lymphocyte The peptide reacts with
 CC lymphocytes from donors with any type of malignancy. It can be used as a
 CC challenging agent in the SCM test which is used to distinguish
 CC lymphocytes isolated from mammals with cancer from those isolated from
 CC donors free of malignancy. It is one of a group of peptides which differ
 CC from each other by 'conservative' amino acid substitutions. (Updated on
 CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
 Score: 17.00 Matches: 2
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-185 (1-9) x AAP91787 (1-8)

Qy 3 TGGGGG 8

Db 3 TrpGly 4

RESULT 11

AAP91784

ID AAP91784 standard; peptide; 8 AA.

XX AC AAP91784;

XX DT 25-MAR-2003 (revised)

XX DT 09-JAN-2003 (revised)

PT antibodies used to provide sensitive assays for detecting malignancy.
XX
PS Disclosure; Page; 40pp; English.
XX
CC matrix (SCM) test; responding lymphocyte The peptide reacts with
CC lymphocytes from donors with any type of malignancy. It can be used as a
CC challenging agent in the SCM test which is used to distinguish
CC lymphocytes isolated from mammals with cancer from those isolated from
CC donors free of malignancy. It is one of a group of peptides which differ
CC from each other by 'conservative' amino acid substitutions. (Updated on
CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 AA;
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x AAP91788 (1-8)
QY 3 TGGGGG 8
DB 3 TrpGly 4
RESULT 14
ID AAP91782 standard; peptide; 8 AA.
XX AAP91782;
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 01-FEB-1990 (first entry)
XX Synthetic SCM-active cancer recognition peptide.
DE Cancer detection; malignancy detection; structuredness of cytoplasmic.
KW Homo sapiens.
XX WO8908118-A.
XX 08-SEP-1989.
PF 01-MAR-1989; 89WO-US000816.
PR 02-MAR-1988; 88US-00163250.
XX (CERC/) CERCEK B.
XX Cerceek B, Cerceek L;
XX WPI: 1989-278286/38.
DR N-PSDB; AAN90948.
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
PT antibodies used to provide sensitive assays for detecting malignancy.
PS Disclosure; Page; 40pp; English.
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
CC lymphocytes from donors with any type of malignancy. It can be used as a
CC challenging agent in the SCM test which is used to distinguish
CC lymphocytes isolated from mammals with cancer from those isolated from
CC donors free of malignancy. It is one of a group of peptides which differ
CC from each other by 'conservative' amino acid substitutions. (Updated on
CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX
SQ Sequence 8 AA;
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x AAP91782 (1-8)
QY 3 TGGGGG 8
DB 3 TrpGly 4
RESULT 15
ID AAP90683 standard; peptide; 8 AA.
XX AAP90683;
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 01-FEB-1990 (first entry)
XX Synthetic SCM-active cancer recognition peptide.
DE Cancer detection; malignancy detection; structuredness of cytoplasmic.
KW Homo sapiens.
XX WO8908118-A.
XX 08-SEP-1989.
PF 01-MAR-1989; 89WO-US000816.
PR 02-MAR-1988; 88US-00163250.
XX (CERC/) CERCEK B.
XX Cerceek B, Cerceek L;
XX WPI: 1989-278286/38.
DR N-PSDB; AAN90940.
XX Synthetic SCM-active cancer recognition peptide(s) - DNA probes and
PT antibodies used to provide sensitive assays for detecting malignancy.
PS Claim 6; Table 2; 40pp; English.
XX matrix (SCM) test; responding lymphocyte The peptide reacts with
CC lymphocytes from donors with any type of malignancy. It can be used as a
CC challenging agent in the SCM test which is used to distinguish
CC lymphocytes isolated from mammals with cancer from those isolated from
CC donors free of malignancy. It is one of a group of peptides which differ
CC from each other by 'conservative' amino acid substitutions. (Updated on
CC 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 AA;
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 17.00 Matches: 2
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-846-033B-185 (1-9) x AAP90683 (1-8)

Qy 3 TGGGG 8
| | | | |
Db 2 TrpGly 3

Search completed: April 11, 2005, 19:00:56
Job time : 51.7273 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:45:50 ; Search time 42.8727 Seconds
(without alignments)
214.995 Million cell updates/sec

Title: US-09-846-033b-184
Perfect score: 18
Sequence: 1 999999gtac 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spool_p/US09846033/runat_11042005_185609_24068/app.query.fasta.1.796
-DB=UniProt -QFMT=fasta -SUFFIX=rup -MINMATCH=0.1 -LDOOPCL=0 -LDOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09846033@cgn 1 1 427 @runat_11042005_185609_24068 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	9	1 DSIP RABIT	P01158 oryctolagus
2	18	100.0	10	2 Q51812	Q51812 plasmod f.
3	18	100.0	12	2 Q9N2B8	Q9N2B8 pongo pygma
4	18	100.0	12	2 Q9N2B9	Q9N2B9 gorilla gor
5	18	100.0	12	2 Q9N2C0	Q9N2C0 pan troglod
6	18	100.0	15	1 PLAS MICAE	P10625 microcytis
7	18	100.0	15	1 UC14_WAIZE	P80620 zea mays (m
8	18	100.0	15	1 VSP1_AGKHP	P80899 agkistrodon
9	18	100.0	15	2 Q7M4Z7	Q7M4Z7 fusarium sp
10	18	100.0	15	2 Q7M4Z8	Q7M4Z8 fusarium sp
11	18	100.0	15	2 Q7M1W8	Q7M1W8 arabidopsis
12	18	100.0	15	2 Q9PRW2	Q9PRW2 crotalus at
13	18	100.0	15	2 Q9PRW3	Q9PRW3 crotalus at
14	18	100.0	15	2 Q97098	Q97098 human immun
15	18	100.0	16	2 Q78510	Q78510 human immun
16	18	100.0	17	2 Q78324	Q78324 human immun

17	18	100.0	17	2	Q78327	Q78327 human immun
18	18	100.0	17	2	Q78378	Q78378 human immun
19	18	100.0	17	2	Q78379	Q78379 human immun
20	18	100.0	17	2	Q78380	Q78380 human immun
21	18	100.0	17	2	Q78381	Q78381 human immun
22	18	100.0	18	2	Q9S8F9	Q9S8F9 populus tre
23	18	100.0	19	1	TLB1_BOTJA	P81882 bothrops ja
24	18	100.0	19	1	TLB2_BOTJA	P81883 bothrops ja
25	18	100.0	19	1	TLB3_BOTJA	P81884 bothrops ja
26	18	100.0	19	2	Q60628	Q60628 mus musculu
27	18	100.0	20	1	VSP1_AGKEI	P33588 agkistrodon
28	18	100.0	20	1	VSP1_TRIOK	P20005 trimeresuru
29	18	100.0	20	2	Q81Z13	Q81Z13 homo sapien
30	18	100.0	20	2	Q7M262	Q7M262 holcus lana
31	18	100.0	20	2	Q9QVG0	Q9QVG0 rattus sp.
32	18	100.0	20	2	Q9PS55	Q9PS55 crotalus at
33	18	100.0	20	2	Q78486	Q78486 human immun
34	18	100.0	20	2	Q78505	Q78505 human immun
35	18	100.0	20	2	Q78507	Q78507 human immun
36	18	100.0	20	2	Q78508	Q78508 human immun
37	18	100.0	21	2	Q9T2V1	Q9T2V1 crithidia f
38	18	100.0	21	2	Q08934	Q08934 nicotiana t
39	18	100.0	21	2	Q923D0	Q923D0 mus musculu
40	18	100.0	21	2	Q9PRW4	Q9PRW4 crotalus at
41	18	100.0	21	2	Q9PS60	Q9PS60 gallus gall
42	18	100.0	21	2	Q78484	Q78484 human immun
43	18	100.0	21	2	Q78503	Q78503 human immun
44	18	100.0	21	2	Q78504	Q78504 human immun
45	18	100.0	22	2	Q726S0	Q726S0 homo sapien

ALIGNMENTS

RESULT 1
DSIP RABIT
ID DSIP RABIT STANDARD; PRT; 9 AA.
AC P01158;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta sleep-inducing peptide (DSIP).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=77185324; PubMed=862769;
RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA Schoenenberger G.A.;
RT "The delta sleep inducing peptide (DSIP). Comparative properties of
the original and synthetic nonapeptide."
RL Experientia 33:548-552(1977).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=79054421; PubMed=568769;
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
analysis, sequence, synthesis and activity of the nonapeptide."
RL Pflugers Arch. 376:119-129(1978).
RN [3]
RP REVIEW.
RX MEDLINE=87175129; PubMed=3550726; DOI=10.1016/0196-9781(86)90148-8;
RA Graf M.V., Kaestlin A.J.;
RT "Delta-sleep-inducing peptide (DSIP): an update."
RL Peptides 7:1165-1187(1986).
CC -!- FUNCTION: When infused into the mesencephalic ventricle of
recipient rabbits induces spindle and delta EEG activity and
reduced motor activities.
CC -!- MISCELLANEOUS: This peptide was obtained from dialysates of
occipital venous sinus blood from rabbits kept asleep by electric
stimulation of the thalamus.
CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 8 of March 2001;

CC WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".

DR PR; A01422; QDRB.
KW Direct protein sequencing.
SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Alignment Scores:
Pred. No.: 1.14e+08 Length: 9
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x DSIP_RABIT (1-9)

Qy 1 GGGGGTGCAC 9
Db 3 GlyGlyAsp 5

RESULT 2

Q51812 Q51812 PRELIMINARY; PRT; 10 AA.
AC Q51812;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DNA helicase (Fragment).

GN Name=trai;
OS Plasmid F.
OG Plasmid F.
OC other sequences; plasmids.
OX NCBI_TaxID=2465;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=92009201; PubMed=1916281; DOI=10.1016/0378-1119(91)90469-R;
RA Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;
RT "Sequence and conservation of genes at the distal end of the transfer region on plasmids F and R6-5.";

RL Gene 104:85-90(1991).
DR EMBL; M38047; AAA98090.1; -.
DR GO; GO:0004386; F.helicase activity; IEA.
KW Helicase; Plasmid.

FT NON TER 1
SQ SEQUENCE 10 AA; 1088 MW; 59A3047731A33B13 CRC64;

Alignment Scores:

Pred. No.: 6.67e+04 Length: 10
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q51812 (1-10)

Qy 1 GGGGGTGCAC 9
Db 8 GlyGlyAsp 10

RESULT 3

Q9N2B8 Q9N2B8 PRELIMINARY; PRT; 12 AA.
AC Q9N2B8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).

GN Name=INMT;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]

RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041365; BAA94453.1; -.
DR GO; GO:0008168; F.methyltransferase activity; IEA.
DR GO; GO:0016740; F.transferase activity; IEA.
KW Methyltransferase; Transferase.

FT NON TER 12
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Alignment Scores:

Pred. No.: 6.67e+04 Length: 12
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q9N2B8 (1-12)

Qy 1 GGGGGTGCAC 9
Db 7 GlyGlyAsp 9

RESULT 4

Q9N2B9 Q9N2B9 PRELIMINARY; PRT; 12 AA.
AC Q9N2B9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).

GN Name=INMT;
OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]

RP SEQUENCE FROM N.A.

RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041364; BAA94453.1; -.

DR GO; GO:0008168; F.methyltransferase activity; IEA.
DR GO; GO:0016740; F.transferase activity; IEA.
KW Methyltransferase; Transferase.

FT NON TER 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Alignment Scores:

Pred. No.: 6.67e+04 Length: 12
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q9N2B9 (1-12)

Qy 1 GGGGGTGCAC 9
Db 7 GlyGlyAsp 9

RESULT 5

Q9N2C0 Q9N2C0 PRELIMINARY; PRT; 12 AA.
AC Q9N2C0;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).

GN Name=INMT;
OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB041363; BAA94452.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Alignment Scores:
Pred. No.: 6.67e+04 Length: 12
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q9N2C0 (1-12)

OY 1 GGGGGTGAC 9

Db 7 GlyGlyAsp 9

RESULT 6

ID PLAS_MICAE STANDARD; PRT; 15 AA.
AC P10625;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Plastocyanin (Fragment).
GN Name=ptcE;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP SEQUENCE
RX MEDLINE=89134784; PubMed=2537099;
RA Tan S., Ho K.-K.;
RT "Purification of an acidic plastocyanin from Microcystis aeruginosa."
RL Biochim. Biophys. Acta 973:111-117(1989).
CC -!- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -!- SIMILARITY: Contains 1 plastocyanin-like domain.
DR PIR; S03353; S03353.
DR HAMAP; MF_00566; -; 1.
DR InterPro; IPR000923; BlueCu 1.
DR PROSITE; PS00196; COPPER_BLUE; PARTIAL.
KW Copper; Direct protein sequencing; Electron transport.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1555 MW; 32B6D462F44F969 CRC64;

Alignment Scores:
Pred. No.: 6.66e+04 Length: 15
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x PLAS_MICAE (1-15)
OY 1 GGGGGTGAC 9

Db 8 GlyGlyAsp 10

RESULT 7

UC14_MAIZE
ID UC14_MAIZE STANDARD; PRT; 15 AA.

AC P80620;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 258)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RA TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.9, its MW is: 34.6 kDa.
DR Maize-2DPAGE; P80620; COLEOPTILE.
DR MaizeDB; 123944; -;
KW Direct protein sequencing.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1564 MW; CF0BBAA0B7DE6658 CRC64;

Alignment Scores:
Pred. No.: 6.66e+04 Length: 15
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x UC14_MAIZE (1-15)

OY 1 GGGGGTGAC 9

Db 3 GlyGlyAsp 5

RESULT 8

VSP3 AGKHP
ID_VSP3 AGKHP STANDARD; PRT; 15 AA.
AC P80899;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ancrod (EC 3.4.21.74) (Venombin A) (Protein C activator) (ACC-C)
DE (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Venom;
RA Hong S.;
RL Submitted (FEB-1997) to Swiss-Prot.
CC -!- FUNCTION: Thrombin-like snake venom serine protease. Activates
CC protein C (By similarity).
CC -!- CATALYTIC ACTIVITY: Selective cleavage of Arg-Xaa bond in
CC fibrinogen, to form fibrin, and release fibrinopeptide A. The
CC specificity of further degradation of fibrinogen varies with
CC species origin of the enzyme.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Snake venom
CC subfamily.
DR InterPro; IPR001254; Peptidase_S1.

DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1642 MW; 03BFE10227CD8CDA CRC64;

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 15
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x VSP3_AGKHP (1-15)

Qy 1 GGGGGTGAC 9

Db 3 GlyGlyAsp 5

RESULT 9

Q7M4Z7 ID Q7M4Z7 PRELIMINARY; PRT; 15 AA.

AC Q7M4Z7; 2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cytochrome c2 (Fragment).

OS Fusarium sporotrichioides.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

OX NCBI_TaxID=5514;

RN [1]

RP SEQUENCE.

RA Chow L.P., Fukaya N., Sugura Y., Ueno Y., Tabuchi K., Tsugita A.;

RL Submitted (OCT-1994) to the PIR data bank.

DR PIR; PA0087; PA0087.

FT NON_TER 1

FT NON_TER 15

SQ SEQUENCE 15 AA; 1576 MW; 37EE5E40C4E886DD CRC64;

Alignment Scores:

Pred. No.: 6.66e+04 Length: 15

Score: 18.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q7M4Z7 (1-15)

Qy 1 GGGGGTGAC 9

Db 2 GlyGlyAsp 4

RESULT 10

Q7M4Z8 ID Q7M4Z8 PRELIMINARY; PRT; 15 AA.

AC Q7M4Z8; 2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cytochrome c1 (Fragment).

OS Fusarium sporotrichioides.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

OX NCBI_TaxID=5514;

RN [1]

RP SEQUENCE.

RA Chow L.P., Fukaya N., Sugura Y., Ueno Y., Tabuchi K., Tsugita A.;

RL Submitted (OCT-1994) to the PIR data bank.

DR PIR; PA0064; PA0064.

FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1545 MW; 2A595E40C4E886DD CRC64;

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 15
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q7M4Z8 (1-15)

Qy 1 GGGGGTGAC 9

Db 2 GlyGlyAsp 4

RESULT 11

Q7M1W8 ID Q7M1W8 PRELIMINARY; PRT; 15 AA.

AC Q7M1W8; 2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Protein QA100030 (Fragment).

OS Arabidopsis thaliana (mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE.

RA Kamo M., Kawakami T., Miyatake N., Tsugita A.;

RL Submitted (JUL-1994) to the PIR data bank.

DR PIR; PA0038; PA0038.

FT NON_TER 1

FT NON_TER 15

SQ SEQUENCE 15 AA; 1461 MW; 2C9508F516BEF185 CRC64;

Alignment Scores:

Pred. No.: 6.66e+04 Length: 15

Score: 18.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q7M1W8 (1-15)

Qy 1 GGGGGTGAC 9

Db 7 GlyGlyAsp 9

RESULT 12

Q9PRW2 ID Q9PRW2 PRELIMINARY; PRT; 15 AA.

AC Q9PRW2; 2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Alpha-FIBRINOGENASE isoform A3 (Fragment).

OS Crotalus atrox (Western diamondback rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OX NCBI_TaxID=8730;

RN [1]

RP SEQUENCE.

RA MEDLINE=94296418; PubMed=8024586;

RA Hung C.C., Chiou S.H.;

RT "Isolation of multiple isoforms of alpha-fibrinogenase from the

Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence

RT homology with ancond, an antithrombotic agent from Malayan viper.";
 RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
 SQ SEQUENCE 15 AA; 1656 MW; 03EFE10227D52FDA CRC64;

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 15
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q9PRW2 (1-15)

QY 1 GGGGGTGAC 9
 Db 3 GlyGlyAsp 5
 RESULT 13
 Q9PRW3 PRELIMINARY; PRT; 15 AA.
 ID Q9PRW3
 AC Q9PRW3;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Alpha-FIBRINOGENASE isoform A2 (Fragment).
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94296418; PubMed=8024586;
 RA Hung C.C., Chlou S.H.;
 RT "Isolation of multiple isoforms of alpha-fibrinogenase from the
 RT Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence
 RT homology with ancond, an antithrombotic agent from Malayan viper.";
 RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
 DR PIR; PC2215; PC2215.
 SQ SEQUENCE 15 AA; 1640 MW; 03EFE10227CA12DA CRC64;

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 15
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q9PRW3 (1-15)

QY 1 GGGGGTGAC 9
 Db 3 GlyGlyAsp 5
 RESULT 14
 Q97098 PRELIMINARY; PRT; 15 AA.
 ID Q97098
 AC Q97098;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Gag polypeptide (Fragment).
 GN Name=gag;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LAI;
 RX MEDLINE=98184535; PubMed=9525623;
 RA Wei Q., Fultz P.N.;

RT "Extensive diversification of human immunodeficiency virus type 1
 RT subtype B strains during dual infection of a chimpanzee that
 RT progressed to AIDS.";
 RL J. Virol. 72:3005-3017(1998).
 DR EMBL; U56897; AAC59307.1; -.
 DR GO; GO:0019012; C:virion; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000071; Retrovir_p17.
 DR Pfam; PF00540; Gag_p17; 1.
 KW AIDS; Core protein; Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1487 MW; 5AC22868622AA49A CRC64;

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 15
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q97098 (1-15)

QY 1 GGGGGTGAC 9
 Db 10 GlyGlyAsp 12
 RESULT 15
 Q78510 PRELIMINARY; PRT; 16 AA.
 ID Q78510
 AC Q78510;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Immunodeficiency virus type 1, viral sample FLQSRG (Florida local
 DE control 01), partial env cds, V5 region. (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92271245; PubMed=1589796;
 RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
 RA Jaffe H.W.;
 RT "Molecular epidemiology of HIV transmission in a dental practice.";
 RL Science 256:1165-1171(1992).
 RN [2]

QY 1 GGGGGTGAC 9
 Db 14 GlyGlyAsp 16
 RESULT 16
 Q78510 PRELIMINARY; PRT; 16 AA.
 ID Q78510
 AC Q78510;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Immunodeficiency virus type 1, viral sample FLQSRG (Florida local
 DE control 01), partial env cds, V5 region. (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92271245; PubMed=1589796;
 RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
 RA Jaffe H.W.;
 RT "Molecular epidemiology of HIV transmission in a dental practice.";
 RL Science 256:1165-1171(1992).
 RN [2]

Alignment Scores:
 Pred. No.: 6.66e+04 Length: 16
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x Q78510 (1-16)

QY 1 GGGGGTGAC 9
 Db 14 GlyGlyAsp 16

Search completed: April 11, 2005, 19:09:47

Job time : 44.8727 secs



J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1343
A;Molecule type: DNA
A;Residues: 1-11 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 1.32e+04 Length: 11
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x PH1343 (1-11)
Qy 1 GGGGGTGAC 9
Db 1 GlyGlyAsp 3

RESULT 3
S60354
retinal oxidase - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S60354
R;Huang, D.Y.; Ichikawa, Y.
Biochim. Biophys. Acta 1243, 431-436, 1995
A;Title: Identification of essential lysyl and cysteinyl residues, and the amino acid sequence of retinal oxidase from rabbit
A;Reference number: S60354; MUID:95244596; PMID:7727518
A;Accession: S60354
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-11 <HUA>

Alignment Scores:
Pred. No.: 1.32e+04 Length: 11
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x S60354 (1-11)
Qy 1 GGGGGTGAC 9
Db 1 GlyGlyAsp 3

RESULT 4
PN0044
protein kinase C inhibitor I - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0044
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cell
A;Reference number: PN0041
A;Accession: PN0044
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked
C;Keywords: brain

Alignment Scores:
Pred. No.: 1.32e+04 Length: 11
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x PN0044 (1-11)
Qy 1 GGGGGTGAC 9
Db 8 GlyGlyAsp 10

RESULT 5
I41946
T-cell receptor gamma chain (5t.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: I41946
R;Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: I41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHB>
C;Keywords: T-Cell receptor

Alignment Scores:
Pred. No.: 1.32e+04 Length: 11
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x I41946 (1-11)
Qy 1 GGGGGTGAC 9
Db 5 GlyGlyAsp 7

RESULT 6
A61575
Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)
N;Alternate names: hemorrhagic toxin
C;Species: Trimeresurus elegans (Sakishima habu)
C;Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: A61575
R;Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.
Int. J. Biochem. 23, 73-78, 1991
A;Title: Isolation and characterization of hemorrhagic toxin from the venom of Trimeresurus
A;Reference number: A61575; MUID:91216327; PMID:2022298
A;Accession: A61575
A;Molecule type: protein
A;Residues: 1-11 <NIK>
C;Keywords: hydrolase; serine proteinase; venom

Alignment Scores:
Pred. No.: 1.32e+04 Length: 11
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x A61575 (1-11)
Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 7
S48210
collagen alpha 1(V) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x E33098 (1-14)

Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 10
PH1598
Ig H chain V-D-J region (wild-type clone 306) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1598
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1598
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Alignment Scores:
Pred. No.: 1.31e+04 Length: 14
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x PH1598 (1-14)

Qy 1 GGGGGTGAC 9
Db 8 GlyGlyAsp 10

RESULT 11
PH0945
T-cell receptor beta chain V-D-J region (clone 16) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0945
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0945
A;Molecule type: mRNA
A;Residues: 1-14 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TTC for residue 11 as Ser
C;Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 1.31e+04 Length: 14
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x PH0945 (1-14)

Qy 1 GGGGGTGAC 9
Db 8 GlyGlyAsp 10

RESULT 12
PC2215

fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N;Alternate names: alpha-fibrinogenase A2
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: PC2215
R;Hung, C.C.; Chiou, S.H.
Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
A;Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamondback viper.
A;Reference number: PC2214; MUID:94296418; PMID:8024586
A;Accession: PC2215
A;Molecule type: protein
A;Residues: 1-15 <HUN>
A;Cross-references: UNIPROT:Q9PRW3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase

Alignment Scores:
Pred. No.: 1.31e+04 Length: 15
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x PC2215 (1-15)
Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 13
S66215
cartilage oligomeric matrix protein - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S66215
R;Hauser, N.; Paulsson, M.; Kale, A.A.; DiCesare, P.E.
FEBS Lett. 368, 307-310, 1995
A;Title: Tendon extracellular matrix contains pentameric thrombospondin-4 (TSP-4).
A;Reference number: S66214; MUID:95354859; PMID:7628627
A;Accession: S66215
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HAU>

Alignment Scores:
Pred. No.: 1.31e+04 Length: 15
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x S66215 (1-15)
Qy 1 GGGGGTGAC 9
Db 9 GlyGlyAsp 11

RESULT 14
E56978
collagen alpha 2(XI) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C;Accession: E56978
R;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ind
A;Reference number: A56978; MUID:95370194; PMID:7642541
A;Accession: E56978
A;Status: preliminary
A;Molecule type: protein

A;Residues: 1-15 <WUA>
A;Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in F5

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Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x E56978 (1-15)
Qy 1 GGGGGTGAC 9
Db 6 GlyGlyAsp 8

RESULT 15
S03353
plastocyanin - Microcystis aeruginosa (fragment)
C;Species: Microcystis aeruginosa
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S03353
R;Tan, S.; Ho, K.K.
Biochim. Biophys. Acta 973, 111-117, 1989
A;Title: Purification of an acidic plastocyanin from Microcystis aeruginosa.
A;Reference number: S03353; MUID:89134784; PMID:2537099
A;Accession: S03353
A;Molecule type: protein
A;Residues: 1-15 <TAN>
A;Cross-references: UNIPROT:P10625

Alignment Scores:
Pred. No.: 1.31e+04 Length: 15
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
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DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x S03353 (1-15)
Qy 1 GGGGGTGAC 9
Db 8 GlyGlyAsp 10

Search completed: April 11, 2005, 19:11:46
Job time : 10.2455 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 19:09:59 ; Search time 35.6727 Seconds
(without alignments)
167.522 Million cell updates/sec

Title: US-09-846-033B-184
Perfect score: 18
Sequence: 1 99999gtgac 9

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 2836020

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications AA -QWMT=fastan -SUFFIX=rapb -MINMATCH=0.1
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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2	18	100.0	8	9	US-09-243-079-13	Sequence 13, Appl
3	18	100.0	8	9	US-09-243-079-14	Sequence 14, Appl
4	18	100.0	8	9	US-09-243-079-15	Sequence 15, Appl
5	18	100.0	8	9	US-09-243-079-16	Sequence 16, Appl
6	18	100.0	8	9	US-09-243-079-17	Sequence 17, Appl
7	18	100.0	8	9	US-09-243-079-18	Sequence 18, Appl
8	18	100.0	8	10	US-09-880-748-3119	Sequence 3119, Ap
9	18	100.0	8	10	US-09-880-748-3214	Sequence 3214, Ap
10	18	100.0	8	14	US-10-022-066-586	Sequence 586, App
11	18	100.0	8	14	US-10-428-826-93	Sequence 93, Appl
12	18	100.0	8	15	US-10-367-555-2	Sequence 2, Appli
13	18	100.0	8	15	US-10-293-418-3119	Sequence 3119, Ap
14	18	100.0	8	15	US-10-293-418-3214	Sequence 3214, Ap
15	18	100.0	8	15	US-10-341-979-4	Sequence 4, Appli
16	18	100.0	8	15	US-10-149-138-1711	Sequence 1711, Ap
17	18	100.0	8	15	US-10-182-252A-202	Sequence 202, App
18	18	100.0	8	15	US-10-182-252A-1205	Sequence 1205, Ap
19	18	100.0	8	16	US-10-149-138-1711	Sequence 1711, Ap
20	18	100.0	8	17	US-10-639-194-41	Sequence 41, Appl
21	18	100.0	9	9	US-09-780-053-358	Sequence 358, App
22	18	100.0	9	9	US-09-780-053-639	Sequence 639, App
23	18	100.0	9	9	US-09-833-948-182	Sequence 182, App
24	18	100.0	9	10	US-09-880-748-2954	Sequence 2954, Ap
25	18	100.0	9	10	US-09-972-656-63	Sequence 63, Appl
26	18	100.0	9	13	US-10-008-355-10	Sequence 10, Appl
27	18	100.0	9	14	US-10-133-210-187	Sequence 187, App
28	18	100.0	9	14	US-10-357-175-68	Sequence 68, Appl
29	18	100.0	9	14	US-10-172-597-182	Sequence 182, App
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31	18	100.0	9	15	US-10-293-418-2954	Sequence 2954, Ap
32	18	100.0	9	15	US-10-245-871-835	Sequence 835, App
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35	18	100.0	9	15	US-10-149-138-1951	Sequence 1951, Ap
36	18	100.0	9	15	US-10-149-138-1969	Sequence 1969, Ap
37	18	100.0	9	15	US-10-447-161-85	Sequence 85, Appl
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39	18	100.0	9	15	US-10-398-104-11	Sequence 11, Appl
40	18	100.0	9	15	US-10-253-286-835	Sequence 835, App
41	18	100.0	9	16	US-10-149-138-726	Sequence 726, App
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43	18	100.0	9	16	US-10-149-138-1951	Sequence 1951, Ap
44	18	100.0	9	16	US-10-149-138-1969	Sequence 1969, Ap
45	18	100.0	9	16	US-10-788-016-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-813-653-41
; Sequence 41, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 41

; FILE REFERENCE: 29928-PCT-USA-I
; CURRENT APPLICATION NUMBER: US/09/243,079
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 08/335,733
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: PCT/IT93/00049
; PRIOR FILING DATE: 1993-05-10
; PRIOR APPLICATION NUMBER: RM92A/000350
; PRIOR FILING DATE: 1992-05-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-243-079-16

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Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-846-033B-184 (1-9) x US-09-243-079-16 (1-8)

Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 6

US-09-243-079-17
; Sequence 17, Application US/09243079
; Patent No. US20020081566A1
; GENERAL INFORMATION:

; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY
; FILE REFERENCE: 29928-PCT-USA-I
; CURRENT APPLICATION NUMBER: US/09/243,079
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 08/335,733
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: PCT/IT93/00049
; PRIOR FILING DATE: 1993-05-10
; PRIOR APPLICATION NUMBER: RM92A/000350
; PRIOR FILING DATE: 1992-05-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-243-079-17

Alignment Scores:
Pred. No.: 8.08e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-846-033B-184 (1-9) x US-09-243-079-17 (1-8)

Qy 1 GGGGGTGAC 9
Db 2 GlyGlyAsp 4

RESULT 7

US-09-243-079-18
; Sequence 18, Application US/09243079

; Patent No. US20020081566A1
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY
; FILE REFERENCE: 29928-PCT-USA-I
; CURRENT APPLICATION NUMBER: US/09/243,079
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 08/335,733
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: PCT/IT93/00049
; PRIOR FILING DATE: 1993-05-10
; PRIOR APPLICATION NUMBER: RM92A/000350
; PRIOR FILING DATE: 1992-05-11
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; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-243-079-18

Alignment Scores:
Pred. No.: 8.08e+07 Length: 8
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-846-033B-184 (1-9) x US-09-243-079-18 (1-8)

Qy 1 GGGGGTGAC 9
Db 1 GlyGlyAsp 3

RESULT 8

US-09-880-748-3119
; Sequence 3119, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3119
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3119

Alignment Scores:
Pred. No.: 8.08e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-846-033B-184 (1-9) x US-09-880-748-3119 (1-8)

Oy 1 GGGGGTGCAC 9
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Db 1 GlyGlyAsp 3

RESULT 9

US-09-880-748-3214
; Sequence 3214, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3214

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Pred. No.: 8.08e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-846-033B-184 (1-9) x US-09-880-748-3214 (1-8)

Oy 1 GGGGGTGCAC 9
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Db 5 GlyGlyAsp 7

RESULT 10

US-10-022-066-586
; Sequence 586, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022.066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 586
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
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; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Unknown amino acid
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; LOCATION: (8)
; OTHER INFORMATION: Unknown amino acid
US-10-022-066-586

Alignment Scores:
Pred. No.: 8.08e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-846-033B-184 (1-9) x US-10-022-066-586 (1-8)

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Db 3 GlyGlyAsp 5

RESULT 11

US-10-428-826-93
; Sequence 93, Application US/10428826
; Publication No. US20030186225A1
; GENERAL INFORMATION:
; APPLICANT: PAUL DR, PREM S
; APPLICANT: ZHANG, YANJIN
; TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
; FILE REFERENCE: 8199-0005-55Xcip WO
; CURRENT APPLICATION NUMBER: US/10/428.826
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/601,326
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/02630
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 09/019,793
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: US 08/478,316
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/301,435
; PRIOR FILING DATE: 1994-09-01
; PRIOR APPLICATION NUMBER: US 08/131,625
; PRIOR FILING DATE: 1993-10-05
; PRIOR APPLICATION NUMBER: US 07/969,071
; PRIOR FILING DATE: 1992-10-30
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Porcine reproductive and respiratory syndrome virus
US-10-428-826-93

Alignment Scores:
Pred. No.: 8.08e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-846-033B-184 (1-9) x US-10-428-826-93 (1-8)

Oy 1 GGGGGTGCAC 9
| | | | |

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Db          2 GlyGlyAsp 4
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; Sequence 2, Application US/10367555
; Publication No. US20030219402A1
; GENERAL INFORMATION:
; APPLICANT: Rutter, William J
; TITLE OF INVENTION: CHIMERIC MOLECULES FOR CLEAVAGE IN A TREATED HOST
; FILE REFERENCE: PRAX-005/01US
; CURRENT APPLICATION NUMBER: US/10/367,555
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/357,740
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: linker containing the enterokinase cleavage site
US-10-367-555-2
Alignment Scores:
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Score:          18.00        Matches:      3
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             15          Gaps:        0
US-09-846-033B-184 (1-9) x US-10-367-555-2 (1-8)
QY          1 GGGGGTGAC 9
Db          2 GlyGlyAsp 4
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US-10-293-418-3119
; Sequence 3119, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3119
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
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; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3119
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3119
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Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
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Db          2 GlyGlyAsp 4
RESULT 14
US-10-293-418-3214
; Sequence 3214, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3214
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QY          1 GGGGGTGAC 9
Db          5 GlyGlyAsp 7
RESULT 15
US-10-341-979-4
; Sequence 4, Application US/10341979
; Publication No. US20040002128A1
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science & Technology
; APPLICANT: Chang, Donald Choy
; APPLICANT: Luo, Qian Kathy
; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
; FILE REFERENCE: 32144183-1
; CURRENT APPLICATION NUMBER: US/10/341,979
; CURRENT FILING DATE: 2003-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
US-10-341-979-4

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US-09-846-033B-184 (1-9) x US-10-341-979-4 (1-8)

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Db      1 GlyGlyasp 3

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Job time : 36.9227 secs
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:49:31 ; Search time 10.5545 Seconds
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Perfect score: 18
Sequence: 1 ggggggtgac 9

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database : Issued Patents AA:*
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	100.0	8	1	US-08-174-365A-32
3	18	100.0	8	1	US-08-487-860-62
4	18	100.0	8	2	US-08-459-568-75
5	18	100.0	8	2	US-08-399-411-75
6	18	100.0	8	2	US-08-244-496-72
7	18	100.0	8	2	US-08-841-483-29
8	18	100.0	8	3	US-08-335-733D-13
9	18	100.0	8	3	US-08-335-733D-14
10	18	100.0	8	3	US-08-335-733D-15
11	18	100.0	8	3	US-08-335-733D-16
12	18	100.0	8	3	US-08-335-733D-17

13	18	100.0	8	3	US-08-335-733D-18	Sequence 18, Appl
14	18	100.0	8	3	US-08-516-859A-75	Sequence 25, Appl
15	18	100.0	8	3	US-09-382-911-29	Sequence 79, Appl
16	18	100.0	8	3	US-09-586-472-75	Sequence 75, Appl
17	18	100.0	8	4	US-09-528-706-75	Sequence 75, Appl
18	18	100.0	8	4	US-09-601-326-93	Sequence 93, Appl
19	18	100.0	8	5	PCT-US95-03236-50	Sequence 50, Appl
20	18	100.0	9	1	US-08-221-226-1	Sequence 1, Appl
21	18	100.0	9	1	US-08-221-226-3	Sequence 3, Appl
22	18	100.0	9	1	US-08-215-805A-4	Sequence 4, Appl
23	18	100.0	9	1	US-08-215-805A-7	Sequence 7, Appl
24	18	100.0	9	1	US-08-215-805A-16	Sequence 16, Appl
25	18	100.0	9	1	US-08-215-805A-20	Sequence 20, Appl
26	18	100.0	9	1	US-08-215-805A-48	Sequence 48, Appl
27	18	100.0	9	1	US-08-215-805A-52	Sequence 52, Appl
28	18	100.0	9	1	US-08-215-805A-57	Sequence 57, Appl
29	18	100.0	9	1	US-08-215-805A-58	Sequence 58, Appl
30	18	100.0	9	1	US-08-215-805A-61	Sequence 61, Appl
31	18	100.0	9	1	US-08-215-805A-74	Sequence 74, Appl
32	18	100.0	9	1	US-08-457-172-1	Sequence 1, Appl
33	18	100.0	9	1	US-08-704-170-48	Sequence 48, Appl
34	18	100.0	9	1	US-08-482-106-3	Sequence 3, Appl
35	18	100.0	9	1	US-08-482-106-5	Sequence 5, Appl
36	18	100.0	9	1	US-08-482-106-7	Sequence 7, Appl
37	18	100.0	9	1	US-08-482-106-9	Sequence 9, Appl
38	18	100.0	9	1	US-08-482-106-11	Sequence 11, Appl
39	18	100.0	9	1	US-08-482-106-13	Sequence 13, Appl
40	18	100.0	9	2	US-08-796-598-1	Sequence 1, Appl
41	18	100.0	9	2	US-08-447-175A-1	Sequence 1, Appl
42	18	100.0	9	2	US-08-747-137-146	Sequence 146, App
43	18	100.0	9	3	US-08-159-339A-1088	Sequence 1088, Ap
44	18	100.0	9	3	US-08-159-339A-1089	Sequence 1089, Ap
45	18	100.0	9	3	US-09-518-046-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-07-968-781A-12
; Sequence 12, Application US/07968781A
; Patent No. 5430137
; GENERAL INFORMATION:
; APPLICANT: Gaertner, Frank H.
; APPLICANT: Sick, August J.
; APPLICANT: Thompson, Mark
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Schwab, George E.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Probes for the Identification of Bacillus
; TITLE OF INVENTION: Thuringiensis Endotoxin Genes
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/968,781A
; FILING DATE: 19921030
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA44.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-968-781A-12

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x US-07-968-781A-12 (1-8)

Qy 1 GGGGGTGAC 9
Db 6 GlyGlyAsp 8

RESULT 2
US-08-174-365A-32
; Sequence 32, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seiichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified site
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note = "Xaa is modified amino acid as
; OTHER INFORMATION: described in specification"
US-08-174-365A-32

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-174-365A-32 (1-8)

Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 3
US-08-487-860-62
; Sequence 62, Application US/08487860
; Patent No. 5792456
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
; FUNCTIONAL EQUIVALENTS REACTIVE WITH HUMAN CARCINOMAS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,860
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.16US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-860-62

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-487-860-62 (1-8)

Qy 1 GGGGGTGAC 9
Db 3 GlyGlyAsp 5

RESULT 4

US-08-459-568-75
; Sequence 75, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-75

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Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-846-033B-184 (1-9) x US-08-459-568-75 (1-8)
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; Sequence 75, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-75

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-399-411-75 (1-8)
QY 1 GGGGGTGAC 9
Db ||||| 6 GlyGlyAsp 8

RESULT 6
US-08-244-496-72
; Sequence 72, Application US/08244496
; Patent No. 5837686
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 85
; COMPUTER READABLE FORM:
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; FILING DATE: 25-NOV-1991
; APPLICATION NUMBER: US/08/244,496
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125024.1
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /product="OTHER"
; OTHER INFORMATION: /note="AMIDATED"
US-08-244-496-72

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Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0
US-09-846-033B-184 (1-9) x US-08-244-496-72 (1-8)			
Qy	1 GGGGGTGCAC 9		
Db	6 GlyGlyAsp 8		
RESULT 7			
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; Sequence 29, Application US/08841483B			
; Patent No. 5976875			
; GENERAL INFORMATION:			
; APPLICANT: Prescott, Steven M.			
; APPLICANT: Bunting, Michaeline			
; APPLICANT: Tang, Wen			
; APPLICANT: Topham, Matthew			
; TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon			
; TITLE OF INVENTION: Methods of Use Thereof			
; FILE REFERENCE: 2037.2.1a			
; CURRENT APPLICATION NUMBER: US/08/841,483B			
; CURRENT FILING DATE: 1997-04-22			
; EARLIER APPLICATION NUMBER: 60/016,210			
; EARLIER FILING DATE: 1996-04-22			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 29			
; LENGTH: 8			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-08-841-483-29			
Alignment Scores:			
Pred. No.:	1.95e+07	Length:	8
Score:	18.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-846-033B-184 (1-9) x US-08-841-483-29 (1-8)			
Qy	1 GGGGGTGCAC 9		
Db	2 GlyGlyAsp 4		
RESULT 8			
US-08-335-733D-13			
; Sequence 13, Application US/08335733D			
; Patent No. 6042831			
; GENERAL INFORMATION:			
; APPLICANT: Beretta, Alberto			
; TITLE OF INVENTION: HIV PROTEIN EPITOPES			
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA			
; NUMBER OF SEQUENCES: 90			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Baker & Botts, L.L.P.			
; STREET: 30 Rockefeller Plaza			
; CITY: New York			
; STATE: NY			
; COUNTRY: U.S.A.			
; ZIP: 10112-0228			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq Version 1.5			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/335,733D			
; FILING DATE: 10-NOV-1994			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-335-733D-13
;
; Alignment Scores:
; Pred. No.: 1.85e+07 Length: 8
; Score: 18.00 Matches: 3
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 3 Gaps: 0
;
; US-09-846-033B-184 (1-9) x US-08-335-733D-13 (1-8)
;
; Qy 1 GGGGGTGAC 9
; Db 6 Glycylasp 8
;
; RESULT 9
; US-08-335-733D-14
; Sequence 14, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:

```

;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-14

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-335-733D-14 (1-8)

QY 1 GGGGGTGAC 9
Db 5 GlyGlyAsp 7

RESULT 10
US-08-335-733D-15
; Sequence 15, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

;
; ORIGINAL SOURCE:
US-08-335-733D-15

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-335-733D-15 (1-8)

QY 1 GGGGGTGAC 9
Db 4 GlyGlyAsp 6

RESULT 11
US-08-335-733D-16
; Sequence 16, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-16

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

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US-09-846-033B-184 (1-9) x US-08-335-733D-16 (1-8)
Qy 1 GGGGTCAC 9
Db 3 GlyGlyAsp 5

RESULT 12
US-08-335-733D-17
; Sequence 17, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-335-733D-17

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-335-733D-17 (1-8)
Qy 1 GGGGTCAC 9
Db 2 GlyGlyAsp 4

RESULT 13
US-08-335-733D-18
; Sequence 18, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-335-733D-18

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-335-733D-18 (1-8)
Qy 1 GGGGTCAC 9
Db 1 GlyGlyAsp 3

RESULT 14
US-08-516-859A-75
; Sequence 75, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
```

STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-75

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-08-516-859A-75 (1-8)

QY 1 GGGGGTGAC 9
Db 6 GlyGlyAsp 8

RESULT 15
US-09-382-911-29
Sequence 29, Application US/09382911
Patent No. 6221658
GENERAL INFORMATION:
APPLICANT: Prescott, Steven M.
APPLICANT: Bunting, Michaeline
APPLICANT: Tang, Wen
APPLICANT: Topham, Matthew
TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Methods of Use Thereof
FILE REFERENCE: 2037.2.1a
CURRENT APPLICATION NUMBER: US/09/382,911
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 08/841,483
PRIOR FILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/016,210
PRIOR FILING DATE: 1996-04-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 29
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-911-29

Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-184 (1-9) x US-09-382-911-29 (1-8)

QY 1 GGGGGTGAC 9
Db 2 GlyGlyAsp 4

Search completed: April 11, 2005, 19:13:59
Job time : 10.5545 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:41:45 ; Search time 50.7273 Seconds
(without alignments)
137.238 Million cell updates/sec

Title: US-09-846-033B-184
Perfect score: 18
Sequence: 1 99999gtgac 9

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/sgn2_1/USPTO spool_p/US09846033/runat_11042005_185608_24062/app.query.fasta_1.796
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09846033 @CGN 1 1 475 @runat 11042005_185608_24062 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq 16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	8	2 AAR37359	Aar37359 Group 5 s
2	18	100.0	8	2 AAR35090	Aar35090 B. thurin
3	18	100.0	8	2 AAR69445	Aar69445 Integrin-
4	18	100.0	8	2 AAR64040	Aar64040 TAN-1511B
5	18	100.0	8	2 AAR78189	Aar78189 B. thurin
6	18	100.0	8	2 ABB76930	Abb76930 Cyclodext
7	18	100.0	8	3 AAB12089	Aab12089 Ad7 cel p
8	18	100.0	8	4 AAM23320	Aam23320 HIV pepti
9	18	100.0	8	4 AAM22317	Aam22317 HIV pepti
10	18	100.0	8	4 AAE00030	Aae00030 Bacillus

11	18	100.0	8	4 ABP16993	Abp16993 HIV B27 s
12	18	100.0	8	4 ABP17721	Abp17721 HIV B58 s
13	18	100.0	8	4 ABP17679	Abp17679 HIV B58 s
14	18	100.0	8	4 AAE01878	Aae01878 Human dia
15	18	100.0	8	5 ABP55898	Abp55898 B15 class
16	18	100.0	8	5 AAM52802	Aam52802 CCR5-bind
17	18	100.0	8	5 ABG97186	Abg97186 Human leu
18	18	100.0	8	5 AAM49462	Aam49462 Olive pol
19	18	100.0	8	5 ABP47203	Abp47203 Human Bly
20	18	100.0	8	5 ABP47108	Abp47108 Human Bly
21	18	100.0	8	5 AAU75240	Aau75240 Active si
22	18	100.0	8	5 AAU75247	Aau75247 Active si
23	18	100.0	8	5 AAU75241	Aau75241 Active si
24	18	100.0	8	5 AAU97465	Aau97465 HIV-1 inf
25	18	100.0	8	6 ADA38428	Ada38428 Linker co
26	18	100.0	8	7 ADC83720	Adc83720 Human mat
27	18	100.0	8	7 ADD15710	Add15710 Peptide 1
28	18	100.0	8	7 ADE84662	Ade84662 Adenoviru
29	18	100.0	8	7 ADG97935	Adg97935 scfV VHCD
30	18	100.0	8	7 ADG98030	Adg98030 scfV VHCD
31	18	100.0	8	7 ADL99022	Adl99022 Human leu
32	18	100.0	8	7 ADM65819	Adm65819 Apoptosis
33	18	100.0	8	8 ADN61402	Adn61402 Paenibaci
34	18	100.0	9	1 AAP82688	Aap82688 Delta sile
35	18	100.0	9	2 AAR07966	Aar07966 Tryptic f
36	18	100.0	9	2 AAR20729	Aar20729 Panceras-
37	18	100.0	9	2 AAR62148	Aar62148 HIV-1 gpl
38	18	100.0	9	2 AAR62365	Aar62365 Delta sile
39	18	100.0	9	2 AAR69457	Aar69457 Integrin-
40	18	100.0	9	2 AAR69475	Aar69475 Integrin-
41	18	100.0	9	2 AAR69444	Aar69444 Integrin-
42	18	100.0	9	2 AAR69477	Aar69477 Integrin-
43	18	100.0	9	2 AAW49545	Aaw49545 Human leu
44	18	100.0	9	2 AAW49533	Aaw49533 Human leu
45	18	100.0	9	2 AAW49532	Aaw49532 Human leu

ALIGNMENTS

RESULT 1
AAR37359
ID AAR37359 standard; peptide; 8 AA.
XX

AC AAR37359;
DT 07-SEP-1993 (first entry)
XX
DE Group 5 synthetic peptide 123.
XX
KW Thiol-active cysteine; antibody; complex; rheumatoid arthritis; therapy;
KW Iga-alpha-antitrypsin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT /note= "amidated"
XX
PN GB2261665-A.
XX
PD 26-MAY-1993.
XX
PF 25-NOV-1992; 92GB-00024684.
XX
PR 25-NOV-1991; 91GB-00025024.
XX
PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.
XX
PI Kirby J, Lewin Iv, Nayyar S, Stanworth Dr;
XX
DR WPI; 1993-169522/21.
XX
PT New synthetic peptide(s) - cause dissociation or prevent formation of IGA

PT -alpha-antitrypsin complex, useful for treating and preventing rheumatoid
PT arthritis.

XX PS Claim 1; Page 28; 38pp; English.

XX CC The peptide is an example of a synthetic peptide contg. a thiol- active
CC cysteine residue and at least two positively charged amino acid residues
CC situated at the N and/or C terminal sides of the thiol- active
CC cysteine. The peptide is pref. amidated at the C- terminus. The peptides
CC may be used in conjunction with an antibody complex comprising a domain
CC specific for an antigenic determinant of a complex of human IgA and alpha
CC -1-antitrypsin, for use in therapy of rheumatoid arthritis. Admin. is
CC oral or parenteral. See also AAR36613-74 and AAR37353-74

XX SQ Sequence 8 AA;

Alignment Scores: Length: 8
Pred. No.: 9.59e+07 Matches: 3
Score: 18.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x AAR37359 (1-8)

QY 1 GGGGGTGCAC 9
| | | | |
Db 6 GlyGlyAasp 8

RESULT 2

AAR35090
ID AAR35090 standard; protein; 8 AA.

XX AC AAR35090;

XX DT 25-MAR-2003 (revised)
XX DT 05-AUG-1993 (first entry)

XX DE B. thuringiensis universal toxin probe (a) design peptide.

XX KW Probe; Bacillus thuringiensis; Bt; insecticidal; active; endotoxin;
XX KW lepidoptera; diptera; coleoptera.

XX OS Synthetic.

XX PN US5204237-A.

XX PD 20-APR-1993.

XX PF 26-JUL-1991; 91US-00737569.

XX PR 25-OCT-1989; 89US-00427068.

XX PA (MYCO) MYCOGEN CORP.

XX PI Gaertner PH, Sick AJ, Schwab GE;

XX WPI; 1993-143952/17.

XX PT Gene probe for identifying endotoxin sequences in Bacillus thuringiensis
PT - are universal, type specific or gene specific, for rapid detection and
PT characterisation of insecticidal activity.

XX PS Disclosure; Col 2; 5pp; English.

XX CC The sequences given in AAR35090-100 and AAR34628-32 are peptides which
CC were used to design the probes given in AA040219-34. These probes can be
CC used to identify Bacillus thuringiensis (Bt) DNA which encodes
CC insecticidally active endotoxin. Probe (a) identifies genes encoding a
CC toxin effective against any sort of insect. Sequences (b) and (e) - (l)
CC are specific for toxins against lepidoptera; sequences (c), (m) and (n)
CC for toxins active against diptera and sequence (d), (o) and (p) for

CC toxins active against coleoptera. (Updated on 25-MAR-2003 to correct PF
CC field.)

XX SQ Sequence 8 AA;

Alignment Scores: Length: 8
Pred. No.: 9.59e+07 Matches: 3
Score: 18.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x AAR35090 (1-8)

QY 1 GGGGGTGCAC 9
| | | | |
Db 6 GlyGlyAasp 8

RESULT 3

AAR69445
ID AAR69445 standard; peptide; 8 AA.

XX AC AAR69445;

XX DT 25-MAR-2003 (revised)

XX DT 27-JUL-1995 (first entry)

XX DE Integrin-inhibiting linear peptide.

XX KW Integrin inhibitor; beta-3 receptor; thrombosis, cardiac infarct;
XX KW arteriosclerosis; angina pectoris; antitumour; osteoporosis;
XX KW angiogenesis; restenosis; angioplasty; wound healing; antimicrobial;
XX KW affinity chromatography.

XX OS Synthetic.

XX PN EP618225-A1.

XX PD 05-OCT-1994.

XX PF 21-MAR-1994; 94EP-00104395.

XX PR 01-APR-1993; 93DE-04310632.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Jonczyk A, Diefenbach B, Felding-Habermann B;

XX WPI; 1994-304404/38.

XX PT New oligopeptide inhibitors of integrin - for treatment and prevention of
XX PT cardiovascular diseases, e.g. thrombosis, or tumours.

XX PS Claim 3; Page 15; 18pp; German.

XX CC The sequence is a specifically claimed example of a group of generically
CC claimed linear peptides which are integrin inhibitors. In particular, the
CC peptides inhibit interaction of the beta-3 integrin receptor with
CC ligands. They can be used in human or veterinary medicine to treat e.g.
CC thrombosis, cardiac infarct, arteriosclerosis, angina pectoris, tumours,
CC osteoporosis, angiogenesis and restenosis after angioplasty. The peptides
CC also stimulate wound healing; are antimicrobials (esp. used with
CC implants, catheters etc.); and can be used to purify integrins by
CC affinity chromatography. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Alignment Scores: Length: 8
Pred. No.: 9.59e+07 Matches: 3
Score: 18.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x AAR69445 (1-8)

QY 1 GGGGGTGAC 9
DB 2 GlyGlyAap 4

RESULT 4
AAR64040
ID AAR64040 standard; peptide; 8 AA.
XX
AC AAR64040;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1995 (first entry)
XX
DE TAN-1511B, an acylated polyhydroxy amino acid-containing polypeptide.
XX
KW Immunostimulant; leukocyte-increasing; leukocytopenia; haematopoiesis;
KW TAN-1511 complex; TAN-1511A; TAN-1511B; TAN-1511C.
XX
OS Streptosporangium sp.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "2-acylamino-6,7-bis(acyloxy)-4-thiaheptanoyl, in
FT which the acyl groups comprise mixed higher fatty acid
FT residues"
XX
PN EP604945-A1.
XX
PD 06-JUL-1994.
XX
PF 27-DEC-1993; 93EP-00120952.
XX
PR 28-DEC-1992; 92JP-00349062.
PR 09-AUG-1993; 93JP-00197579.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Tanida S, Hida T, Wakimasu M;
XX
XX WPI; 1994-210208/26.
XX
PT New amino-acyl derivs. of peptide(s), designated TAN-1511 - useful as
PT immunostimulating agents having leukocyte-increasing activity and
PT increasing bone marrow cell proliferation.
XX
PS Claim 13; Page 59; 66pp; English.
XX
CC Novel peptides are disclosed which have at the 1-position a 2- acylamino-
CC 6,7-di(aliphatic acyloxy)-4-thiaheptanoic acid residue and which have an
CC additional 2-8 amino acids, at least one of which is acidic. The acyl
CC groups are pref. higher aliphatic acyl groups, pref. n-hexadecanoyl (Pam)
CC or n-tetradecanoyl (Myr). The peptides can be synthesised; but mixtures
CC of them, designated TAN-1511 complex, can also be obtained by culturing
CC Streptosporangium AU-234546. The complex comprises components 151A,
CC 151B and 151C (see also AAR64039 and AAR64041), each of which has a
CC unique peptide chain and all of which have a mixture of higher fatty acid
CC acyl groups on the 1-position amino acid. The peptides have
CC immunostimulating and leukocyte-increasing activity and can be used for
CC therapy or prophylaxis of leukocytopenia (caused by radiotherapy or
CC chemotherapy of cancers), as a haematopoiesis stimulator in bone marrow
CC transplantation, and as an immunological enhancing agent for increasing
CC leukocytes. This sequence is that of TAN-1511B. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x AAR64040 (1-8)

QY 1 GGGGGTGAC 9
DB 3 GlyGlyAap 5

RESULT 5
AAR78189
ID AAR78189 standard; peptide; 8 AA.
XX
AC AAR78189;
XX
DT 25-MAR-2003 (revised)
DT 22-FEB-1996 (first entry)
XX
DE B. thuringiensis endotoxin derived peptide.
XX
KW Endotoxin; probe; microbes; peptide; detection; coleopteran;
KW lepidopteran; mite; dipteran.
XX
OS Bacillus thuringiensis.
XX
PN US5430137-A.
XX
PD 04-JUL-1995.
XX
PF 30-OCT-1992; 92US-00968781.
XX
PR 25-OCT-1989; 89US-00427068.
PR 26-JUL-1991; 91US-00737569.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Thompson M, Schnepf HE, Schwab GE, Gaertner FH, Narva KE;
PI Sick AJ;
XX
DR WPI; 1995-245777/32.
DR P-PSDB; AAQ91782.
XX
PT Nucleotide sequence used as probes to identify Bacillus thuringiensis -
PT are derived from the B.thuringiensis endotoxin genes, for identifying
PT microbes which encode toxins.
XX
PS Example 2; Col 23-24; 30pp; English.
XX
CC The nucleotide sequence which encodes AAR78189, a B. thuringiensis (B.t.)
CC endotoxin derived peptide, is the probe AAQ91782. The probe can be used
CC for the detection of endotoxin producing B.t. microbes. The probe aids in
CC the search for useful microbes hosting toxin encoding genes, specifically
CC from coleopteran, lepidopteran, mite and dipteran species. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-184 (1-9) x AAR78189 (1-8)

QY 1 GGGGGTGAC 9

```

Db          |||||
            6 GlyGlyAsp 8
RESULT 6
ABB76930
ID ABB76930 standard; peptide; 8 AA.
XX
XX
AC ABB76930;
XX
XX 16-JUL-2002 (first entry)
DT
XX Cyclodextrin glucanotransferase-related peptide #11.
DE
XX Cyclodextrin glucanotransferase; microorganism.
KW
XX
XX OS
XX Unidentified.
XX
XX KR9704943-B1.
PN
XX
XX 10-APR-1997.
PD
XX
XX 01-SEP-1993; 93KR-00017341.
PF
XX
XX 08-SEP-1992; 92KR-00016335.
PR
XX
XX (JONG-) JONGKNDANG CO LTD.
PA
XX (KOG-) KOREA GENETIC ENG RES ASSOC.
XX
XX Yang H, Lee K, Jung K, Min K, Lim S;
PI
XX WPI; 1999-455124/38.
DR
XX
XX Novel gene of cyclodextrin glucanotransferase from microorganism and
PT vector and recombinant transformants.
XX
XX Claim 9; Page 11; 15pp; Korean.
PS
XX
XX The present invention relates to the cyclodextrin glucanotransferase gene
CC from a microorganism and related vector and recombinant transformants.
CC The present peptide was used to illustrate the invention
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-846-033B-184 (1-9) x ABB76930 (1-8)
Qy 1 GGGGGTGAC 9
Db 1 GlyGlyAsp 3
RESULT 7
AAB12089
ID AAB12089 standard; peptide; 8 AA.
XX
XX
AC AAB12089;
XX
XX 12-SEP-2003 (revised)
DT
XX 17-JAN-2001 (first entry)
DT
XX
XX Ad7 cel peptide.
DE
XX
XX Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;
KW cell proliferation; cell differentiation; tissue repair;
KW transcription regulator; breast cancer; gene therapy; melanoma;
KW neuroblastoma; leukaemia; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; paralysis; motor neurone disorder; cel.

```

```

XX OS unidentified adenovirus.
XX PN US6069231-A.
XX 30-MAY-2000.
XX
XX 18-AUG-1995; 95US-00516859.
XX
XX 18-AUG-1994; 94US-00292683.
PR 06-MAR-1995; 95US-00399411.
XX
XX (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX Huang S;
PI
XX WPI; 2000-410879/35.
DR
XX
XX New PR domain peptides comprising amino acid sequences from, for example
PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for
PT regulating gene transcription and controlling cell proliferation and
PT differentiation.
XX
XX Disclosure; Fig 2; 91pp; English.
PS
XX
XX The present sequence is Ad7 cel from Adenovirus. The cel domain is also
CC found in rat retinoblastoma (Rb)-interacting zinc finger (RIZ) protein
CC (AAB12028). RIZ is a nuclear phosphoprotein that acts as a cell
CC differentiation factor. RIZ can modulate cell growth by binding to Rb
CC protein, which is involved in regulating cell proliferation. In addition,
CC RIZ can act to regulate transcription. RIZ functions to maintain cells in
CC the G1 phase of the cell cycle, by interacting with Rb through the cr2
CC domain of RIZ. Rat RIZ protein contains a number of GTPase motifs (see
CC AAB12037 to AAB12056 and AAB12099 to AAB12104). RIZ protein is a PR
CC domain protein and is present primarily in the cell nucleus. RIZ gene
CC mutations may be implicated in various cancers such as melanoma,
CC neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be
CC used in gene therapy for these disorders. Since RIZ protein is implicated
CC in cell cycle arrest, inhibition of RIZ activity may be useful in
CC neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's or
CC Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
CC disorders e.g. heart disease, where the ability to induce neural/ cardiac
CC tissue proliferation would be useful. The present sequence was used for
CC sequence homology comparison. (Updated on 12-SEP-2003 to standardise OS
CC field)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-846-033B-184 (1-9) x AAB12089 (1-8)
Qy 1 GGGGGTGAC 9
Db 6 GlyGlyAsp 8
RESULT 8
AAM23320
ID AAM23320 standard; peptide; 8 AA.
XX
XX
AC AAM23320;
XX
XX 22-OCT-2001 (first entry)
DT
XX HIV peptide SEQ ID NO 1205.
DE
XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
KW

```

KW human immunodeficiency virus; vaccine.

XX OS Human immunodeficiency virus.
OS Synthetic.

PN WO200155177-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-DK000059.

XX PR 28-JAN-2000; 2000EP-00610017.

XX PR 31-JAN-2000; 2000US-0179333P.

XX PA (STAT-) STATENS SERUM INST.

XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;

XX DR WPI; 2001-476184/51.

XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in anti-HIV vaccines.

XX PS Example 4; Page 358; 383pp; English.

XX CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or prevent infection of cells in the host, but CTL will limit viral production by killing the cell. The CTL epitopes are useful in medicine, CC in the manufacture of vaccines or diagnostic agents

XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x AAM23320 (1-8)

OY 1 GGGGGTGAC 9

DB 2 GlyGlyAsp 4

RESULT 9

AAM22317

ID AAM22317 standard; peptide; 8 AA.

XX AC AAM22317;

XX DT 22-OCT-2001 (first entry)

XX DE HIV peptide SEQ ID NO 202.

XX KW Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;

XX OS human immunodeficiency virus; vaccine.

XX OS Human immunodeficiency virus.

XX OS Synthetic.

XX PN WO200155177-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-DK000059.

XX PR 28-JAN-2000; 2000EP-00610017.

XX PR 31-JAN-2000; 2000US-0179333P.

XX (STAT-) STATENS SERUM INST.

XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;

XX DR WPI; 2001-476184/51.

XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in anti-HIV vaccines.

XX PS Claim 13; Page 55; 383pp; English.

XX CC The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or prevent infection of cells in the host, but CTL will limit viral production by killing the cell. The CTL epitopes are useful in medicine, CC in the manufacture of vaccines or diagnostic agents

XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x AAM22317 (1-8)

OY 1 GGGGGTGAC 9

DB 2 GlyGlyAsp 4

RESULT 10

AAE00030

ID AAE00030 standard; peptide; 8 AA.

XX AC AAE00030;

XX DT 11-SEP-2003 (revised)

XX DT 31-MAY-2001 (first entry)

XX DE Bacillus strain C3371 peptide to design 646 sense primer.

XX KW Residual protease II; RP-II; additive; cleaning composition; detergent.

XX OS Bacillus sp; C3371.

XX PN WO200116285-A2.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-DK000476.

XX PR 31-AUG-1999; 99DK-00001212.

XX PR 20-OCT-1999; 99DK-00001500.

XX PA (NOVO) NOVOZYMES AS.

XX PI Norregaard-Madsen M, Rahbek Ostergaard P, Voge Christensen CB;

XX PI Flensted Lassen S;

XX DR WPI; 2001-226680/23.

XX PT Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions.

XX PS Example 1; Page 69; 132pp; English.

XX CC The present sequence is Bacillus strain C3371 RP-II (Residual protease

CC II) peptide used to design 646 sense primer (AAD03019). RP-II protease is
 CC useful as a constituent in additives, detergent compositions and other
 CC cleaning compositions, optionally in combination with other enzymes such
 CC as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The
 CC variants of RP-II have improved properties such as substrate
 CC specificities, catalytic rate, stability, especially towards the action
 CC of proteolytic enzymes and improved resistance towards peroxidase.
 CC (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x AAE00030 (1-8)

QY 1 GGGGGTGAC 9
 ID | | | | | | | |
 DB 4 GlyGlyAsp 6

RESULT 11
 ABP16993
 ID ABP16993 standard; peptide; 8 AA.

XX AC ABP16993;

DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)

XX HIV B27 super motif env peptide #18.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 217; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTI), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x ABP16993 (1-8)

QY 1 GGGGGTGAC 9
 ID | | | | | | | |
 DB 5 GlyGlyAsp 7

RESULT 12

ABP17721

ID ABP17721 standard; peptide; 8 AA.

XX AC ABP17721;

DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)

XX HIV B58 super motif env peptide #122.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 232; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x ABP17721 (1-8)

QY 1 GGGGGTGAC 9

DB 3 GlyGlyAsp 5

RESULT 13

ABP17679

ID ABP17679 standard; peptide; 8 AA.

XX ABP17679;

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

DE HIV B58 super motif env peptide #80.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

OS WO200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPTM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 231; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 18.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x ABP17679 (1-8)

QY 1 GGGGGTGAC 9

DB 3 GlyGlyAsp 5

RESULT 14

AAE01878

ID AAE01878 standard; peptide; 8 AA.

XX AAE01878;

DT 31-JUL-2001 (first entry)

XX Human diacylglycerol kinase (DGK) alpha peptide (residues 432-439).

XX Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;
 KW diacylglycerol kinase alpha; DGK.

XX Homo sapiens.

XX US6221658-B1.

XX 24-APR-2001.

XX 25-AUG-1999; 99US-00382911.

XX 22-APR-1996; 96US-0016210P.

XX 22-APR-1997; 97US-00841483.

XX (UTAH) UNIV UTAH RES FOUND.

XX Prescott SM, Bunting M, Tang W, Topham M;

XX WPI; 2001-327248/34.

XX New DNAs of the human diacylglycerol kinase, useful for modulating the
 PT levels of diacylglycerol kinase in cells to catalyze the conversion of
 PT diacylglycerol to phosphatidic acid, therefore increasing phosphatidic
 PT acid levels.

XX Example 2; Col 22; 74pp; English.

XX The patent discloses novel human diacylglycerol kinase (DGK) isoforms
 CC namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta,

CC diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human
CC diacylglycerol kinase DNA is useful for coding human diacylglycerol
CC kinase, which is useful for catalysing the conversion of diacylglycerol
CC to phosphatidic acid. In particular, the human diacylglycerol kinase and
CC its DNA are useful for decreasing intracellular levels of diacyl-
CC glycerol (DAG) and for increasing intracellular levels of phosphatidic
CC acid in cells. The present sequence is a peptide of human diacylglycerol
CC kinase (DGK) alpha (residues 432-439). The forward RT-PCR primer
CC (AAG05702) based on this sequence is used to amplify human DGK alpha cDNA
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-184 (1-9) x AAE01878 (1-8)

Qy 1 GGGGGTGAC 9
Db 2 GlyGlyAsp 4

RESULT 15

ABP55898
ID ABP55898 standard; peptide; 8 AA.

AC ABP55898;

XX 25-FEB-2003 (first entry)

XX B15 class I sHLA molecule ligand related peptide #192.

XX HLA ligand; human leukocyte antigen; predictive algorithm; database;
KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.

XX Synthetic.

XX WO200269198-A2.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US005298.

XX 21-FEB-2001; 2001US-0270357P.

PR 10-OCT-2001; 2001US-00974366.

PR 18-DEC-2001; 2001US-00022066.

XX (HILD/) HILDEBRAND W H.

PA (PRIL/) PRILLIMAN K R.

PA (HICK/) HICKMAN H D.

XX Hildebrand WH, Prilliman KR, Hickman HD;

XX WPI; 2002-732755/79.

XX Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.

PS Disclosure; Fig 5; 118pp; English.

XX The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated

CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands
CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 18.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-846-033B-184 (1-9) x ABP55898 (1-8)

Qy 1 GGGGGTGAC 9

Db 3 GlyGlyAsp 5

Search completed: April 11, 2005, 19:00:55
Job time : 52.7273 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:45:50 ; Search time 90.5091 Seconds
(without alignments)
214.995 Million cell updates/sec

Title: US-09-846-033B-183
Perfect score: 35
Sequence: 1 atggacgggtgagcgccg 19

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spool_p/US09846033/runat_11042005_185609_24068/app_query.fasta.1.796
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LDOPECL=0 -LDOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09846033 @CGN 1 1 427 @runat_11042005_185609_24068 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	82	Q8WT04	Q8WT04 plasmodium
2	35	100.0	276	Q881K0	Q881K0 pseudomonas
3	35	100.0	297	Q9R2K1	Q9R2K1 incw plasm
4	35	100.0	318	Q616B2	Q616B2 escherichia
5	35	100.0	592	Q8A6K2	Q8A6K2 bacteroides
6	35	100.0	613	Q8G9C7	Q8G9C7 azocarcus sp
7	35	100.0	729	Q747L0	Q747L0 geobacter s
8	35	100.0	65	Q751Z3	Q751Z3 oryza sativ
9	33	100.0	88	Q61PM3	Q61PM3 homo sapien
10	33	100.0	93	Q649L0	Q649L0 uncultured
11	33	100.0	102	Q6MY73	Q6MY73 aspergillus
12	33	100.0	118	Q6E073	Q6E073 oryza sativ
13	33	100.0	129	Q9RTG0	Q9RTG0 deinococcus
14	33	100.0	132	Q6ERR5	Q6ERR5 oryza sativ
15	33	100.0	136	PS12 PANTR	Q7YR45 pan troglod
16	33	100.0	136	Q9PGP9	Q9PGP9 xyliella fas

C 17	33	100.0	137	2	Q84ZJ2	Q84ZJ2 oryza sativ
C 18	33	100.0	142	2	Q6ZVY2	Q6ZVY2 homo sapien
C 19	33	100.0	145	2	Q6VMP4	Q6VMP4 oryza sativ
C 20	33	100.0	154	2	Q827B1	Q827B1 streptomyce
C 21	33	100.0	172	2	Q8BY28	Q8BY28 m mus muscu
C 22	33	100.0	173	2	Q8NAG1	Q8NAG1 homo sapien
C 23	33	100.0	180	2	Q7XQA3	Q7XQA3 oryza sativ
C 24	33	100.0	182	2	Q656C1	Q656C1 oryza sativ
C 25	33	100.0	186	2	Q6Q299	Q6Q299 sorghum bic
C 26	33	100.0	186	2	Q6Q2A0	Q6Q2A0 sorghum bic
C 27	33	100.0	186	2	Q9LLG3	Q9LLG3 jankaea hel
C 28	33	100.0	187	2	Q8FFH8	Q8FFH8 xanthomonas
C 29	33	100.0	192	2	Q8DMP9	Q8DMP9 synectococ
C 30	33	100.0	196	2	Q6H6S8	Q6H6S8 oryza sativ
C 31	33	100.0	201	2	Q9CVP8	Q9CVP8 mus musculu
C 32	33	100.0	204	2	Q7XDD0	Q7XDD0 oryza sativ
C 33	33	100.0	204	2	Q9FWH7	Q9FWH7 oryza sativ
C 34	33	100.0	208	2	Q9CVW7	Q9CVW7 mus musculu
C 35	33	100.0	211	2	Q41506	Q41506 sorghum bic
C 36	33	100.0	212	2	Q41295	Q41295 sorghum bic
C 37	33	100.0	217	2	Q6AAB7	Q6AAB7 propionibac
C 38	33	100.0	222	2	Q8YNR1	Q8YNR1 anabaena sp
C 39	33	100.0	225	2	Q83692	Q83692 treponema p
C 40	33	100.0	229	2	Q7Z2S3	Q7Z2S3 homo sapien
C 41	33	100.0	229	2	Q6UNJ0	Q6UNJ0 schlumberge
C 42	33	100.0	230	1	VHEL P1AMV	Q07517 plantago as
C 43	33	100.0	232	2	Q8S2Z7	Q8S2Z7 oryza sativ
C 44	33	100.0	235	2	Q02442	Q02442 globodera r
C 45	33	100.0	243	2	Q7S8Z7	Q7S8Z7 neurospora

ALIGNMENTS

RESULT 1
Q8WT04 PRELIMINARY; PRT; 82 AA.
ID Q8WT04
AC Q8WT04;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI TaxID=5861;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YM;
RA Bayele H.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ301639; CAC82904.1; -.
KW Hypothetical protein.
FT NON_TER 82
SQ SEQUENCE 82 AA; 9416 MW; 6F25D38ADC9556C3 CRC64;

Alignment Scores:
Pred. No.: 162 Length: 82
Score: 35.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q8WT04 (1-82)

QY 2 TGGACGGGTGAGCGGCG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 32 TrpThrGlyGluAlaAla 37

RESULT 2

Q881K0 PRELIMINARY; PRT; 276 AA.
ID Q881K0
AC Q881K0;
DT 01-JUN-2003 (Tremblrel. 24, Created)

DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	PAP2 superfamily protein.
GN	OrderedLocusNames=PSPTO2893;
OS	Pseudomonas syringae (pv. tomato).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;	
[1]	
RP	SEQUENCE FROM N.A.
RC	STRAIN=DC3000;
RX	MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA	Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA	Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA	Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA	Nelson W.C., Davidse T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA	Khourii H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA	Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA	Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA	Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA	Bender C.L., White O., Fraser C.M., Collmer A.;
RT	"The complete genome sequence of the Arabidopsis and tomato pathogen
RT	Pseudomonas syringae pv. tomato DC3000.";
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR	EMBL; AE016866; AA056386.1; -.
DR	TIGR; PSPTO2893; -.
DR	InterPro; IPR008934; AcPase_VanPerase.
KW	Complete proteome.
SQ	SEQUENCE 276 AA; 31550 MW; 6B820BA063839C65 CRC64;
Alignment Scores:	
Pred. No.:	168
Score:	35.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
US-09-846-033B-183 (1-19) x Q881K0 (1-276)	
QY	2 TGACGGGTGAGCGGC 19
Db	69 TrpThrGlyAlaAala 74
RESULT 3	
Q9R2K1	
ID	Q9R2K1 PRELIMINARY; PRT; 297 AA.
AC	Q9R2K1;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	ArdC antirestriction protein.
GN	Name=ardC;
OS	Incw plasmid psa.
OC	other sequences; broad host range plasmids.
NCBI_TaxID=102264;	
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20232510; PubMed=10696096; DOI=10.1006/jmbi.1999.3493;
RA	Belogurov A.A., Delver E.P., Agafonova O.V., Belogurova N.G.,
RA	Lee L.Y., Kado C.I.;
RT	"Antirestriction protein Ard (Type C) encoded by Incw plasmid psa has
RT	a high similarity to the 'protein transport' domain of TraCI primase
RT	of promiscuous plasmid RP4.";
RL	J. Mol. Biol. 296:969-977(2000).
DR	EMBL; AF143206; AAD52160.1; -.
SQ	SEQUENCE 297 AA; 33202 MW; 464A047BEE1A946A CRC64;
Alignment Scores:	
Pred. No.:	168
Score:	35.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
US-09-846-033B-183 (1-19) x Q881K0 (1-276)	
QY	2 TGACGGGTGAGCGGC 19
Db	69 TrpThrGlyAlaAala 74
RESULT 3	
Q9R2K1	
ID	Q9R2K1 PRELIMINARY; PRT; 297 AA.
AC	Q9R2K1;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	ArdC antirestriction protein.
GN	Name=ardC;
OS	Incw plasmid psa.
OC	other sequences; broad host range plasmids.
NCBI_TaxID=102264;	
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20232510; PubMed=10696096; DOI=10.1006/jmbi.1999.3493;
RA	Belogurov A.A., Delver E.P., Agafonova O.V., Belogurova N.G.,
RA	Lee L.Y., Kado C.I.;
RT	"Antirestriction protein Ard (Type C) encoded by Incw plasmid psa has
RT	a high similarity to the 'protein transport' domain of TraCI primase
RT	of promiscuous plasmid RP4.";
RL	J. Mol. Biol. 296:969-977(2000).
DR	EMBL; AF143206; AAD52160.1; -.
SQ	SEQUENCE 297 AA; 33202 MW; 464A047BEE1A946A CRC64;
Alignment Scores:	
Pred. No.:	168
Score:	35.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
US-09-846-033B-183 (1-19) x Q881K0 (1-276)	
QY	2 TGACGGGTGAGCGGC 19
Db	69 TrpThrGlyAlaAala 74
RESULT 3	
Q9R2K1	
ID	Q9R2K1 PRELIMINARY; PRT; 297 AA.
AC	Q9R2K1;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	ArdC antirestriction protein.
GN	Name=ardC;
OS	Incw plasmid psa.
OC	other sequences; broad host range plasmids.
NCBI_TaxID=102264;	
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20232510; PubMed=10696096; DOI=10.1006/jmbi.1999.3493;
RA	Belogurov A.A., Delver E.P., Agafonova O.V., Belogurova N.G.,
RA	Lee L.Y., Kado C.I.;
RT	"Antirestriction protein Ard (Type C) encoded by Incw plasmid psa has
RT	a high similarity to the 'protein transport' domain of TraCI primase
RT	of promiscuous plasmid RP4.";
RL	J. Mol. Biol. 296:969-977(2000).
DR	EMBL; AF143206; AAD52160.1; -.
SQ	SEQUENCE 297 AA; 33202 MW; 464A047BEE1A946A CRC64;
Alignment Scores:	
Pred. No.:	168
Score:	35.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
US-09-846-033B-183 (1-19) x Q881K0 (1-276)	
QY	2 TGACGGGTGAGCGGC 19
Db	6

DR InterPro; IPR004634; Pept_S49_SppA67.
 DR Pfam; PF01343; Peptidase_S49; 2.
 DR PIRSF; PIRSF001217; Protease_4_SppA; 1.
 DR ProDom; PD002897; Peptidase_S49; 2.
 DR TIGRFAMs; TIGR00705; SppA_67k; 1.
 DR TIGRFAMs; TIGR00706; SppA_dom; 1.
 KW Complete proteome; Protease.
 SQ SEQUENCE 592 AA; 65407 MW; 97E70CE53B4736E6 CRC64;

Alignment Scores:
 Pred. No.: 171 Length: 592
 Score: 35.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q8A6K2 (1-592)

QY 2 TCGACGGGTGAGCGGCG 19
 Db 496 TrpThrGlyGluAlaAa 501
 RESULT 6
 Q8G9C7 PRELIMINARY; PRT; 613 AA.
 AC Q8G9C7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Protease IV.
 OS Azococcus sp. (strain EbN1).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
 OC Rhodocyclaceae; Azococcus.
 OX NCBI_TaxID=76114;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EbN1;
 RX MEDLINE=22306571; PubMed=12420173;
 RA Rabus R., Kube M., Beck A., Widdel F., Reinhardt R.;
 RT "Genes involved in the anaerobic degradation of ethylbenzene in a
 RT denitrifying bacterium, strain EbN1.";
 RL Arch. Microbiol. 178:506-516(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EbN1;
 RA PROSCIENCE;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL844858; CAD58329.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0009003; P:signal peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006465; P:signal peptide processing; IEA.
 DR InterPro; IPR002142; Peptidase_S49.
 DR InterPro; IPR004635; Pept_S49_SppA67.
 DR InterPro; IPR004634; Pept_S49_SppA67.
 DR PIRSF; PIRSF001217; Protease_4_SppA; 1.
 DR ProDom; PD002897; Peptidase_S49; 2.
 DR TIGRFAMs; TIGR00705; SppA_67k; 1.
 DR TIGRFAMs; TIGR00706; SppA_dom; 1.
 KW Protease.
 SQ SEQUENCE 613 AA; 65724 MW; EDCD183D7DBC1652 CRC64;

Alignment Scores:
 Pred. No.: 171 Length: 613
 Score: 35.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q8G9C7 (1-613)

QY 2 TCGACGGGTGAGCGGCG 19
 Db 508 TrpThrGlyGluAlaAa 513

RESULT 7
 Q747L0 PRELIMINARY; PRT; 729 AA.
 AC Q747L0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=GSU3255;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Winn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 RT environments.";
 RL Science 302:1967-1969(2003).
 DR EMBL; AB017180; AAR36646.1; -.
 DR TIGR; GSU3255; -
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR004300; Glyco_hydro_57.
 DR Pfam; PF03065; Glyco_hydro_57; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 729 AA; 82773 MW; 354FD13E1203AF6A CRC64;

Alignment Scores:
 Pred. No.: 172 Length: 729
 Score: 35.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q747L0 (1-729)

QY 2 TCGACGGGTGAGCGGCG 19
 Db 152 TrpThrGlyGluAlaAa 157

RESULT 8
 Q751Z3 PRELIMINARY; PRT; 65 AA.
 AC Q751Z3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNBa0039N21.11.
 GN Name=OSJNBa0039N21.11;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.J., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC120529; AAS07050.1; -;
KW Hypothetical protein.
SQ SEQUENCE 65 AA; 7461 MW; FB00C475923D7D58 CRC64;

Alignment Scores:
Pred. No.: 426 Length: 65
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q751Z3 (1-65)
Qy 17 CCGCCTCACCGTCC 3
Db 5 ProProHisProSer 9

RESULT 9
Q6IPM3 PRELIMINARY; PRT; 88 AA.
ID Q6IPM3
AC Q6IPM3, 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071857; AAH71857.1; -;
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0030833; P:regulation of actin filament polymerization; IEA.
DR InterPro; IPR006789; p16 Arc.
DR Pfam; PF04699; p16-Arc; I.

KW Hypothetical protein.
SQ SEQUENCE 88 AA; 9403 MW; 8B619003BE5BACBB CRC64;

Alignment Scores:
Pred. No.: 430 Length: 88
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q6IPM3 (1-88)
Qy 17 CCGCCTCACCGTCC 3
Db 55 ProProHisProSer 59

RESULT 10
Q649L0 PRELIMINARY; PRT; 93 AA.
ID Q649L0
AC Q649L0; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZJ4H9_35;
OS uncultured archaeon GZfos34H9.
OC Archaea; environmental samples.
OX NCBI_TaxID=285375;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RL genomics."
RL Science 305:1457-1462 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY714862; AAU83917.1; -;
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10578 MW; 8383CB8013AD2431 CRC64;

Alignment Scores:
Pred. No.: 430 Length: 93
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q649L0 (1-93)
Qy 17 CCGCCTCACCGTCC 3
Db 76 ProProHisProSer 80

RESULT 11
Q6MW73 PRELIMINARY; PRT; 102 AA.
ID Q6MW73
AC Q6MW73; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AfA33H4_105;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]

```

RP SEQUENCE FROM N.A.
RX PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;
RA Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,
RA Foster N., Fraser A., Harris D., Larke N., Murphy L., Humphray S.,
RA O'Neil S., Pettea M., Price C., Rabinowitsch E., Rajandream M-A.,
RA Salzberg S., Saunders D., Seegar K., Sharp S., Warren T.,
RA Denning D.W., Barrell B., Hall N.;
RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922
RT kb region encompassing the nitrate assimilation gene cluster.";
RL Fungal Genet. Biol. 41:443-453(2004).
DR EMBL: BX649607; CAF32130.1; -.
KW Hypothetical protein.
SQ SEQUENCE 102 AA; 11739 MW; 17928D7344F874A7 CRC64;

Alignment Scores:
Pred. No.: 431 Length: 102
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q6MY73 (1-102)

QY 17 CCGCCTCACCCGTC 3
Db 54 ProProHisProSer 58

RESULT 12
Q6EQ73 PRELIMINARY; PRT; 118 AA.
ID Q6EQ73 434 Length: 129
AC Q6EQ73 33.00 Matches: 5
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNB0095I04.15)
DE OSUNB0095I04.15)
GN Name=OSJNB0017118.9; Synonyms=OSJNB0095I04.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005724; BAD29197.1; -.
DR EMBL; AP005701; BAD29129.1; -.
KW Hypothetical protein.
SQ SEQUENCE 118 AA; 12420 MW; 8CD2A607DF8F047D CRC64;

Alignment Scores:
Pred. No.: 433 Length: 118
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q6EQ73 (1-118)

QY 17 CCGCCTCACCCGTC 3
Db 42 ProProHisProSer 46

RESULT 13
Q9RTG0 PRELIMINARY; PRT; 129 AA.
ID Q9RTG0 434 Length: 129
AC Q9RTG0 33.00 Matches: 5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

```

DE Hypothetical protein DR1804.
GN OrderedLocNames=DR1804;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Mofat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE002021; AAF11357.1; -.
DR PIR; H75351; H75351.
DR TIGR; DR1804; -.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003313; AraC binding.
DR InterPro; IPR007113; Cupin region.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 129 AA; 14279 MW; F710E9AB571104FB CRC64;

Alignment Scores:
Pred. No.: 434 Length: 129
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q9RTG0 (1-129)

QY 17 CCGCCTCACCCGTC 3
Db 7 ProProHisProSer 11

RESULT 14
Q6ERR5 PRELIMINARY; PRT; 132 AA.
AC Q6ERR5 434 Length: 132
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0701F11.20 (Hypothetical protein
DE P0668D04.1).
GN Name=P0701F11.20; Synonyms=P0668D04.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
RT clone:P0668D04.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005429; BAD28655.1; -.
DR EMBL; AP005426; BAD33481.1; -.
KW Hypothetical protein.
SQ SEQUENCE 132 AA; 15540 MW; B04D078E4808314D CRC64;

```

Alignment Scores:
 Pred. No.: 435 Length: 132
 Score: 33.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x Q6ERR5 (1-132)

Qy 17 CCGCTCACCGTCC 3
 Db 57 ProProHisProSer 61

RESULT 15

PS12_PANTR
 ID PS12_PANTR STANDARD; PRT; 136 AA.
 AC Q7YR45;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Psoriasis susceptibility 1 candidate gene 2 protein homolog precursor
 DE (SPR1 protein).
 GN Name=PSORS1C2; Synonyms=SPR1;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230531100;
 RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
 RA Yamagata T., Kuleski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
 RA Yamazaki M., Tashiro H., Iwamoto C., Umebara Y., Imanishi T.,
 RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
 RT "Comparative sequencing of human and chimpanzee MHC class I regions
 RT unveils insertions/deletions as the major path to genomic
 RT divergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB100083; BAC78169.1; --
 KW Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 136 Psoriasis susceptibility 1 candidate gene
 FT 2 protein homolog.
 SQ SEQUENCE 136 AA; 15084 MW; 31D44EFED8ADF8A7 CRC64;

Alignment Scores:
 Pred. NO.: 435 Length: 136
 Score: 33.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-846-033B-183 (1-19) x PS12_PANTR (1-136)

Qy 17 CCGCTCACCGTCC 3
 Db 66 ProProHisProSer 70

Search completed: April 11, 2005, 19:09:45
 Job time : 93.5091 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:46:20 ; Search time 19.5182 Seconds
(without alignments)
187.325 Million cell updates/sec

Title: US-09-846-033B-183
Perfect score: 35
Sequence: 1 atggacgggtgagcgccg 19

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2.1/USPTO spool_p/US09846033/runat_11042005_185610_24081/app_query.fasta_1.796
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09846033 @CN 1 1 107 @runat_11042005_185610_24081 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33	100.0	129	2 H75351	conserved hypotet
C 2	33	100.0	136	2 D82830	hypothetical prote
C 3	33	100.0	212	2 S51798	gamma-kafirin prec
C 4	33	100.0	222	2 AE2368	phosphate regulon
C 5	33	100.0	225	2 C71293	probable 5,10-meth
C 6	33	100.0	230	2 S34231	hypothetical prote
C 7	33	100.0	247	2 T31204	hypothetical prote
C 8	33	100.0	264	2 S60367	transcription fact
C 9	33	100.0	270	2 I50111	Dlx2 homeodomain p
C 10	33	100.0	304	2 A32993	transcription fact
C 11	33	100.0	304	2 D70370	hypothetical prote
C 12	33	100.0	326	2 A52332	ABA-responsive pro
C 13	33	100.0	328	2 H75445	conserved hypotet
C 14	33	100.0	385	1 S29844	transforming prote

C 15	33	100.0	415	1 B64089	diaminopimelate de
C 16	33	100.0	452	1 I37565	transforming prote
C 17	33	100.0	465	2 T48374	UDPG glucosyltrans
C 18	33	100.0	466	2 T20647	hypothetical prote
C 19	33	100.0	473	2 H87641	sensor histidine k
C 20	33	100.0	476	2 T41879	AcMNPV orf142 - Bo
C 21	33	100.0	477	2 H72867	early 49 kDa prote
C 22	33	100.0	479	2 T46318	hypothetical prote
C 23	33	100.0	483	2 A84698	probable RNA-bindi
C 24	33	100.0	504	2 A53286	acetyl-CoA C-acety
C 25	33	100.0	544	2 I55454	neuroglycan C prec
C 26	33	100.0	581	2 E59322	dolichol-P-glucose
C 27	33	100.0	582	2 T51625	MAP3K alpha protei
C 28	33	100.0	589	2 T39299	hypothetical prote
C 29	33	100.0	594	2 G96525	protein TIN15.25 l
C 30	33	100.0	608	2 G96575	probable MEK kinas
C 31	33	100.0	631	2 T35234	probable secreted
C 32	33	100.0	637	1 QQVZ11	early transcriptio
C 33	33	100.0	637	2 E42515	D6R protein - vacc
C 34	33	100.0	637	2 T37379	VEF-1, early tran
C 35	33	100.0	637	2 T28534	hypothetical prote
C 36	33	100.0	637	2 C36847	early transcriptio
C 37	33	100.0	637	2 F72162	P6R protein - vari
C 38	33	100.0	650	2 T04487	hypothetical prote
C 39	33	100.0	699	2 A96529	hypothetical prote
C 40	33	100.0	751	2 T34490	hypothetical prote
C 41	33	100.0	771	2 S35681	ESG protein - mous
C 42	33	100.0	772	2 D56695	transducin-like en
C 43	33	100.0	918	2 B84580	hypothetical prote
C 44	33	100.0	922	1 S54342	protein-tyrosine-p
C 45	33	100.0	963	2 AF2119	hypothetical prote

ALIGNMENTS

RESULT 1

H75351
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75351
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Dodson, R.J.;
M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75351
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <WHI>
A:Cross-references: UNIPROT:Q9RTG0; GB:AE002021; GB:AE005513; NID:G6459573; PIDN:AAF1131;
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1804
A:Map position: 1

Alignment Scores:	82.8	Length:	129
Pred. No.:	33.00	Matches:	5
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	2	Gaps:	0
DB:			

US-09-846-033B-183 (1-19) x H75351 (1-129)

Oy 17 CCGCCTCACCGTCC 3
|||||
Db 7 PROPHISPROSER 11
|||||

RESULT 2

D82830

hypothetical protein XF0249 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82830
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82830
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <SIM>
A;Cross-references: UNIPROT:Q9PGP9; GB:AE003878; GB:AE003849; NID:G9105052; PIDN:AAF8306
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0249

Alignment Scores:
Pred. No.: 82.7 Length: 136
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x D82830 (1-136)
Qy 17 CCGCCTCACCGTCC 3
Db 107 ProProHisProSer 111

RESULT 3
S51798
gamma-kafirin precursor - sorghum
N;Alternate names: gamma-prolamin
C;Species: Sorghum bicolor (sorghum)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: S51798; S71784; S70853
R;de Freitas, F.A.; Yunes, J.A.; da Silva, M.J.; Arruda, P.; Leite, A.
Mol. Gen. Genet. 245, 177-186, 1994
A;Title: Structural characterization and promoter activity analysis of the gamma-kafirin
A;Reference number: S51798; MUID:95115665; PMID:7816025
A;Accession: S51798
A;Molecule type: DNA
A;Residues: 1-212 <DEF1>
A;Cross-references: UNIPROT:Q41506; EMBL:X62480
A;Note: the source is designated as Sorghum vulgare
A;Accession: S71784
A;Molecule type: protein
A;Residues: 20-25 <DEF2>
R;Leite, A.
submitted to the EMBL Data Library, October 1991
A;Reference number: S70853
A;Accession: S70853
A;Molecule type: DNA
A;Residues: 1-13,15-212 <LE1>
A;Cross-references: EMBL:X62480; NID:G671655; PIDN:CAA44347.1; PID:G671656
A;Note: the source is designated as Sorghum vulgare

C;Superfamily: glutelin
C;Keywords: seed; storage protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-212/Product: gamma-kafirin #status experimental <MAT>

Alignment Scores:
Pred. No.: 81.4 Length: 212
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x S51798 (1-212)
Qy 17 CCGCCTCACCGTCC 3
Db 82 ProProHisProSer 86

RESULT 4
AE2368
phosphate regulon transcription regulator all4501 [imported] - Nostoc sp. (strain PCC 71
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2368
R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q8YNR1; GB:BA000019; PIDN:BA076200.1; PID:G17133637; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4501
C;Superfamily: phoU protein

Alignment Scores:
Pred. No.: 81.3 Length: 222
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x AE2368 (1-222)
Qy 17 CCGCCTCACCGTCC 3
Db 121 ProProHisProSer 125

RESULT 5
C71293
probable 5,10-methenyltetrahydrofolate synthetase - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: C71293
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: C71293
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-225 <COL>
A;Cross-references: UNIPROT:O83692; GB:AE001243; GB:AE000520; NID:G3322990; PIDN:AAC6566
A;Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0694

Alignment Scores:
Pred. No.: 81.2 Length: 225
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x C71293 (1-225)

Qy 17 CCGCTCACCGTCC 3

Db 121 ProProHisProSer 125

RESULT 6

S34231

hypotheical protein, 25K - Plantago asiatica mosaic virus

C:Species: Plantago asiatica mosaic virus

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S34231

R:Atabekov, J.G.

submitted to the EMBL Data Library, February 1993

A:Reference number: S34230

A:Accession: S34231

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-230 <ATA>

A:Cross-references: UNIPROT:Q07517; EMBL:Z21647; NID:G311644; PIDN:CAA79762.1; PID:G3116

C:Superfamily: potato virus 25K protein

Alignment Scores:

Pred. No.: 81.2 Length: 230
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x S34231 (1-230)

Qy 17 CCGCTCACCGTCC 3

Db 225 ProProHisProSer 229

RESULT 7

T31204

hypotheical protein 659 - Sphingomonas aromaticivorans plasmid pNL1

C:Species: Sphingomonas aromaticivorans

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T31204

R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G

submitted to the EMBL Data Library, July 1998

A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic

A:Reference number: Z20992

A:Accession: T31204

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-247 <ROM>

A:Cross-references: UNIPROT:O85913; EMBL:AF079317; NID:G3378261; PID:G3378345; PIDN:AA00

C:Genetics:

A:Genome: plasmid pNL1

A>Note: orf659

Alignment Scores:

Pred. No.: 81 Length: 247
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x T31204 (1-247)

Qy 17 CCGCTCACCGTCC 3

Db 48 ProProHisProSer 52

RESULT 8

S60367

transcription factor PU.1 homolog - human

N:Alternate names: transforming protein spi-1 homolog

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: S60367; S10892; S60369

R:Ray, D.; Culine, S.; Tavittian, A.; Moreau-Gachelin, F.

submitted to the EMBL Data Library, September 1993

A:Description: The human homologue of the putative proto-oncogene Spi-1: characterization and

A:Reference number: S60367

A:Accession: S60367

A:Molecule type: mRNA

A:Residues: 1-264 <RAY>

A:Cross-references: UNIPROT:P17947; EMBL:X52056; NID:G36560; PIDN:CAA36281.1; PID:G36561

A>Note: this is a revision to the sequence from reference S10892

R:Ray, D.; Culine, S.; Tavittian, A.; Moreau-Gachelin, F.

Oncogene 5, 663-668, 1990

A>Title: The human homologue of the putative proto-oncogene Spi-1: characterization and

A:Reference number: S10892; MUID:90265606; PMID:1693183

A:Accession: S10892

A:Molecule type: DNA

A:Residues: 1-204, 'TAGASRRATARR' <RAW>

A:Cross-references: EMBL:X52056

A>Note: this sequence has been revised in reference S60367

A:Accession: S60369

A:Molecule type: DNA

A:Residues: 1-204, 'TAGASRRATARR' <RAW2>

A:Cross-references: EMBL:X52056

A>Note: this sequence has been revised in reference S60367

C:Genetics:

A:Gene: spi-1

A:Introns: 9/3; 42/1; 104/3; 159/1

C:Superfamily: mouse transcription factor PU.1; ets DNA-binding domain homology

F166-247/Domain: ets DNA-binding domain homology <ETS>

Alignment Scores:

Pred. No.: 80.8 Length: 264
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x S60367 (1-264)

Qy 17 CCGCTCACCGTCC 3

Db 96 ProProHisProSer 100

RESULT 9

I50111

Dlx2 homeodomain protein - zebra fish

N:Alternate names: distal-less X2 protein

C:Species: Brachydanio rerio (zebra fish)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

C:Accession: I50111

R:Akimenko, M.A.; Ekter, M.; Wegner, J.; Lin, W.; Westerfield, M.

J. Neurosci. 14, 3475-3486, 1994

A>Title: Combinatorial expression of three zebrafish genes related to distal-less: part

A:Reference number: I50111; MUID:94267510; PMID:7911517

A:Accession: I50111

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-270 <AKI>

A:Cross-references: UNIPROT:P50574; EMBL:U03875; NID:G460126; PIDN:AAA19826.1; PID:G4601

C;Genetics:

A;Gene: dlx2
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;124-180/Domain: homeobox homology <HOX>

Alignment Scores:
Pred. No.: 80.7 Length: 270
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x I50111 (1-270)

Qy 17 CCGCCTCACCGTCC 3

Db 199 ProProHisProSer 203

RESULT 10

A32993
transcription factor GATA-1 - chicken
N;Alternate names: transcription factor Eryf1
C;Species: Gallus gallus (chicken)
C;Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 09-Jul-2004
C;Accession: A32993
R;Evans, T.; Felsenfeld, G.
Cell 58, 877-885, 1989
A;Title: The erythroid-specific transcription factor Eryf1: a new finger protein.
A;Reference number: A32993; MUID:89376538; PMID:2776214
A;Accession: A32993
A;Molecule type: mRNA
A;Residues: 1-304 <EVA>
A;Cross-references: UNIPROT:P17678; GB:M26209; NID:g212628; PIDN:AAA49055.1; PID:g212629
C;Superfamily: transcription factor GATA-1; GATA-type zinc finger homology
C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc f
F;107-160/Domain: GATA-type zinc finger homology <GF1>
F;110-134/Region: zinc finger GATA motif
F;161-214/Domain: GATA-type zinc finger homology <GF2>
F;164-188/Region: zinc finger GATA motif

Alignment Scores:
Pred. No.: 80.4 Length: 304
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x A32993 (1-304)

Qy 17 CCGCCTCACCGTCC 3

Db 87 ProProHisProSer 91

RESULT 11

hypoetical protein aq_808 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70370
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70370
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-304 <AQF>
A;Cross-references: UNIPROT:O66991; GB:AE000708; NID:g2983356; PIDN:AAC06955.1; PID:g298
A;Experimental source: strain VF5

C;Genetics:

A;Gene: aq_808
C;Superfamily: Aquifex aeolicus hypothetical protein aq_808

Alignment Scores:
Pred. No.: 80.4 Length: 304
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x D70370 (1-304)

Qy 17 CCGCCTCACCGTCC 3

Db 122 ProProHisProSer 126

RESULT 12

A59232
ABA-responsive protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59232
R;Liu, J.H.; Luo, M.; Mohapatra, S.S.
submitted to GenBank, September 1997
A;Reference number: A59232
A;Accession: A59232
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-326 <LIU>
A;Cross-references: UNIPROT:Q9ZTW0; GB:AF026538; NID:g4103634; PIDN:AAD09343.1; PID:g410
A;Experimental source: dev stage embryo
C;Superfamily: barley ABA-responsive protein

Alignment Scores:
Pred. No.: 80.2 Length: 326
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x A59232 (1-326)

Qy 17 CCGCCTCACCGTCC 3

Db 62 ProProHisProSer 66

RESULT 13

H75445
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75445
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.W.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <WHI>
A;Cross-references: UNIPROT:Q9RVK5; GB:AE001954; GB:AE000513; NID:g6458751; PIDN:AAF1059
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1022
A;Map position: 1

Alignment Scores:
Pred. No.: 80.2 Length: 328

Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x H75445 (1-328)

QY 17 CCGCCTCACCGTCC 3
Db 180 ProProHisProSer 184

RESULT 14
S29844
transforming protein fli, short splice form - human
N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 23-May-1997 #text_change 16-Jul-1999
C:Accession: S29844
R:Hronas, R.; May, W.; Denny, C.; Raskind, W.; Moore, J.; Maki, R.A.; Beck, E.; Klemasz, B.; Chochim. Biophys. Acta 1172, 155-158, 1993
A:Title: Human FLI-1 localizes to chromosome 11Q24 and has an aberrant transcript in neuroblastoma
A:Reference number: S29843; MUID:93176799; PMID:8439553
A:Accession: S29844
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-385 <HRO>
A:Cross-references: EMBL:M93255; NID:g18265; PIDN:AAA58480.1; PID:g182661
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1992
C:Genetics:
A:Gene: GDB:FLI1
A:Cross-references: GDB:127565; OMIM:193067
A:Map position: 11q24.1-11q24.3
C:Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regulatory domain homology
C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factor
F:52-126/Domain: ets RII regulatory region homology <ETR>
F:1217-295/Domain: ets DNA-binding domain homology <ETS>

Alignment Scores:
Pred. No.: 79.7 Length: 385
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-183 (1-19) x S29844 (1-385)

QY 17 CCGCCTCACCGTCC 3
Db 336 ProProHisProSer 340

RESULT 15
B64089
diaminopimelate decarboxylase (EC 4.1.1.20) - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B64089
R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64089
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-415 <TIGR>
A:Cross-references: UNIPROT:P44316; GB:U32756; GB:L42023; NID:g1573729; PIDN:AAC22385.1;
C:Superfamily: diaminopimelate decarboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase; pyridoxal phosphate

Alignment Scores:
Pred. No.: 79.5 Length: 415
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-183 (1-19) x B64089 (1-415)

QY 17 CCGCCTCACCGTCC 3
Db 249 ProProHisProSer 253

Search completed: April 11, 2005, 19:11:45
Job time : 21.5182 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:49:31 ; Search time 22.2818 Seconds
(without alignments)
127.308 Million cell updates/sec

Title: US-09-846-033B-183

Perfect score: 35

Sequence: 1 atggacgggtgagcgccg 19

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+n2p.model -runat 11042005 185610 24092/app_query.fasta_1.796
-O=/cgn2_1/USPTO_spool_p/US09846033/runat 11042005 185610 24092/app_query.fasta_1.796
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOFCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUTS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33	100.0	15	2	US-08-553-257A-35
C 2	33	100.0	15	4	US-09-441-992-35
C 3	33	100.0	18	4	US-09-390-134B-37
C 4	33	100.0	55	4	US-09-621-976-5030
C 5	33	100.0	79	4	US-09-248-796A-26832
C 6	33	100.0	88	4	US-09-270-767-37184
C 7	33	100.0	88	4	US-09-270-767-37184
C 8	33	100.0	106	4	US-09-205-258-769
C 9	33	100.0	137	4	US-09-893-737-104
C 10	33	100.0	205	4	US-09-252-991A-17234
C 11	33	100.0	275	4	US-09-902-540-12996
C 12	33	100.0	279	4	US-09-252-991A-29821

C 13	33	100.0	321	3	US-09-417-286-4	Sequence 4, Appli
C 14	33	100.0	452	2	US-08-343-443B-4	Sequence 4, Appli
C 15	33	100.0	455	4	US-09-270-767-35242	Sequence 35242, A
C 16	33	100.0	461	4	US-09-270-767-50459	Sequence 50459, A
C 17	33	100.0	465	4	US-09-422-936-57	Sequence 57, Appl
C 18	33	100.0	467	3	US-09-046-736-2	Sequence 2, Appli
C 19	33	100.0	470	4	US-09-252-991A-19467	Sequence 19467, A
C 20	33	100.0	470	4	US-09-949-016-10559	Sequence 10559, A
C 21	33	100.0	471	3	US-09-311-636B-8	Sequence 8, Appli
C 22	33	100.0	515	3	US-08-796-899-23	Sequence 23, Appl
C 23	33	100.0	631	3	US-09-311-636B-16	Sequence 16, Appl
C 24	33	100.0	638	4	US-09-248-796A-18750	Sequence 18750, A
C 25	33	100.0	640	4	US-09-949-016-10499	Sequence 10499, A
C 26	33	100.0	640	4	US-09-949-016-10500	Sequence 10500, A
C 27	33	100.0	640	4	US-09-949-016-10501	Sequence 10501, A
C 28	33	100.0	640	4	US-09-949-016-10502	Sequence 10502, A
C 29	33	100.0	784	4	US-09-740-235-1	Sequence 1, Appli
C 30	33	100.0	787	4	US-09-252-991A-19991	Sequence 19991, A
C 31	33	100.0	844	4	US-09-422-936-47	Sequence 47, Appl
C 32	33	100.0	844	4	US-09-422-936-51	Sequence 51, Appl
C 33	33	100.0	844	4	US-09-719-085A-4	Sequence 4, Appli
C 34	33	100.0	979	3	US-08-514-213A-2	Sequence 2, Appli
C 35	33	100.0	979	4	US-09-015-399-5	Sequence 5, Appli
C 36	33	100.0	1003	4	US-09-949-016-11260	Sequence 11260, A
C 37	33	100.0	2972	3	US-09-579-181-2	Sequence 2, Appli
C 38	33	100.0	3118	3	US-09-579-181-1	Sequence 1, Appli
C 39	31	93.9	61	4	US-09-248-796A-24993	Sequence 24993, A
C 40	31	88.6	106	4	US-09-621-976-5411	Sequence 5411, Ap
C 41	31	93.9	125	2	US-08-891-848-16	Sequence 16, Appl
C 42	31	93.9	125	3	US-08-875-811-11	Sequence 11, Appl
C 43	31	93.9	125	6	5171845-2	Patent No. 5171845
C 44	31	93.9	125	6	5171845-2	Patent No. 5171845
C 45	31	93.9	133	4	US-09-519-232-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-08-553-257A-35
; Sequence 35, Application US/08553257A
; Patent No. 5994083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.
; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESS: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.257A
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/IT94/00054
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: recombinant protein
; HYPOTHETICAL: yes
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: of recombinant peptides on phage
; CLONE: phagic
; NAME/KEY: polypeptide
; IDENTIFICATION METHOD: selection with specific antibodies
; US-08-553-257A-35
;
Alignment Scores:
Pred. No.: 66.2 Length: 15
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
;
US-09-846-033B-183 (1-19) x US-08-553-257A-35 (1-15)
;
Qy 17 CCGCTCACCGTCC 3
Db 8 ProProHisProSer 12
;
RESULT 2
; Sequence 35, Application US/09441992
; Patent No. 6541210
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; MOLECOLARE P. ANGELETTI S.p.A.
; FELICI, Franco
; LUZZAGO, Alessandra
; NICOSIA, Alfredo
; MONACI, Paolo
; CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
;
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/441,992
FILING DATE: 18-No. 6541210-1999
CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: 08/553,257
FILING DATE: <Unknown>
APPLICATION NUMBER: RM93A000301
FILING DATE: 11-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: recombinant protein
HYPOTHETICAL: yes
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
LIBRARY: of recombinant peptides on phage
CLONE: phagic
NAME/KEY: polypeptide
IDENTIFICATION METHOD: selection with specific antibodies
US-09-441-992-35
;
Alignment Scores:
Pred. No.: 66.2 Length: 15
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
;
US-09-846-033B-183 (1-19) x US-09-441-992-35 (1-15)
;
Qy 17 CCGCTCACCGTCC 3
Db 8 ProProHisProSer 12
;
RESULT 3
; Sequence 37, Application US/09390134B
; Patent No. 6518399
; GENERAL INFORMATION:
; APPLICANT: BARNES, ASHLEY A.
; APPLICANT: WISE, ALAN
; APPLICANT: MARSHALL, FIONA H.
; APPLICANT: FRASER, NEIL J.
; APPLICANT: WHITE, JULIE H. M.
; APPLICANT: FOORD, STEVEN M.
; TITLE OF INVENTION: NOVEL RECEPTOR
; FILE REFERENCE: PG3558US2
; CURRENT APPLICATION NUMBER: US/09/390,134B
; CURRENT FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: GB9819420.2
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-390-134B-37
;
Alignment Scores:
Pred. No.: 66.9 Length: 18
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-390-134B-37 (1-18)

QY 17 CCGCCTCACCGTCC 3
Db 14 ProProHisProSer 18

RESULT 4

US-09-621-976-5030
; Sequence 5030, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5030
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5030

Alignment Scores:
Pred. No.: 71.6 Length: 55
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-621-976-5030 (1-55)

QY 17 CCGCCTCACCGTCC 3
Db 46 ProProHisProSer 50

RESULT 5

US-09-248-796A-26832
; Sequence 26832, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26832
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26832

Alignment Scores:
Pred. No.: 73.1 Length: 79
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-248-796A-26832 (1-79)

QY 17 CCGCCTCACCGTCC 3
Db 23 ProProHisProSer 27

RESULT 6

US-09-270-767-37184
; Sequence 37184, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37184
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37184

Alignment Scores:
Pred. No.: 73.6 Length: 88
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-270-767-37184 (1-88)

QY 17 CCGCCTCACCGTCC 3
Db 47 ProProHisProSer 51

RESULT 7

US-09-270-767-52401
; Sequence 52401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52401
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52401

Alignment Scores:
Pred. No.: 73.6 Length: 88
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-270-767-52401 (1-88)

QY 17 CCGCCTCACCGTCC 3
Db 47 ProProHisProSer 51

RESULT 8

US-09-205-258-769
; Sequence 769, Application US/09205258
; Patent No. 6525174

GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 769
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-769

Alignment Scores:
Pred. No.: 74.4 Length: 106
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-205-258-769 (1-106)

Qy 17 CCGCCTCACCGTCC 3
Db 92 ProProHisProSer 96
|||||

RESULT 9

US-09-893-737-104
; Sequence 104, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-104

Alignment Scores:
Pred. No.: 75.6 Length: 137
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-893-737-104 (1-137)

Qy 17 CCGCCTCACCGTCC 3
Db 81 ProProHisProSer 85
|||||


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RESULT 10
US-09-252-991A-17234
; Sequence 17234, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17234
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17234

Alignment Scores:
Pred. No.: 77.4 Length: 205
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-252-991A-17234 (1-205)
Qy 17 CCGCCTCACCGTCC 3
Db 21 ProProHisProSer 25

RESULT 11
US-09-902-540-12996
; Sequence 12996, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12996
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12996

Alignment Scores:
Pred. No.: 79.8 Length: 275
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-902-540-12996 (1-275)
Qy 17 CCGCCTCACCGTCC 3
Db 74 ProProHisProSer 78

RESULT 12
US-09-252-991A-29821
; Sequence 29821, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29821
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29821

Alignment Scores:
Pred. No.: 78.8 Length: 279
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-252-991A-29821 (1-279)
Qy 17 CCGCCTCACCGTCC 3
Db 9 ProProHisProSer 13

RESULT 13
US-09-417-286-4
; Sequence 4, Application US/09417286
; Patent No. 6306656
; GENERAL INFORMATION:
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Chen, Tein-Chin
; TITLE OF INVENTION: PLANT EMBRYO - AND ALEURONE-SPECIFIC PROMOTER
; FILE REFERENCE: 08919-019001
; CURRENT APPLICATION NUMBER: US/09/417,286
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-417-286-4

Alignment Scores:
Pred. No.: 79.5 Length: 321
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-417-286-4 (1-321)
Qy 17 CCGCCTCACCGTCC 3
Db 62 ProProHisProSer 66

RESULT 14
US-08-343-443B-4
; Sequence 4, Application US/08343443B
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```
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Bearice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; TITLE OF INVENTION: TRANSLATIONS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-343-443B-4

Alignment Scores:
Pred. No.: 81.1 Length: 452
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x US-08-343-443B-4 (1-452)

Oy 17 CCGCCTCACCGTCC 3
Db 402 ProProHisProSer 406

RESULT 15
US-09-270-767-35242
; Sequence 35242, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35242
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35242

Alignment Scores:
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Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-270-767-35242 (1-455)

Oy 17 CCGCCTCACCGTCC 3
Db 396 ProProHisProSer 400

Search completed: April 11, 2005, 19:13:59
Job time : 23.2818 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 19:09:59 ; Search time 75.3091 Seconds
(without alignments)
167.522 Million cell updates/sec

Title: US-09-846-033B-183

Perfect score: 35

Sequence: 1 atggacgggtgagcgccg 19

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delopt 6.0, Delext 7.0

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 2836020

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications AA:
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	35	100.0	239	15	US-10-425-114-69587	Sequence 69587, A
2	33	100.0	18	14	US-10-300-616-37	Sequence 37, Appl
3	33	100.0	47	10	US-09-986-480-200	Sequence 200, App
4	33	100.0	47	17	US-10-863-332-200	Sequence 200, App
5	33	100.0	49	9	US-09-864-761-40279	Sequence 40279, A
6	33	100.0	58	15	US-10-424-599-152461	Sequence 152461, A
7	33	100.0	63	14	US-10-106-698-6126	Sequence 6126, Ap
8	33	100.0	65	15	US-10-424-599-214599	Sequence 214599, A
9	33	100.0	65	16	US-10-437-963-180710	Sequence 180710, A
10	33	100.0	65	16	US-10-767-701-59921	Sequence 59921, A
11	33	100.0	72	15	US-10-424-599-201841	Sequence 201841, A
12	33	100.0	72	15	US-10-424-599-214619	Sequence 214619, A
13	33	100.0	72	15	US-10-424-599-272894	Sequence 272894, A
14	33	100.0	76	16	US-10-437-963-162599	Sequence 162599, A
15	33	100.0	76	16	US-10-437-963-170570	Sequence 170570, A
16	33	100.0	78	15	US-10-424-599-231285	Sequence 231285, A
17	33	100.0	79	11	US-09-864-408A-8888	Sequence 8888, Ap
18	33	100.0	83	15	US-10-424-599-263963	Sequence 263963, A
19	33	100.0	90	16	US-10-437-963-120335	Sequence 120335, A
20	33	100.0	91	15	US-10-264-049-4179	Sequence 4179, Ap
21	33	100.0	92	15	US-10-424-599-157781	Sequence 157781, A
22	33	100.0	93	16	US-10-437-963-195202	Sequence 195202, A
23	33	100.0	100	16	US-10-437-963-141958	Sequence 141958, A
24	33	100.0	104	9	US-09-925-297-599	Sequence 599, App
25	33	100.0	106	10	US-09-933-767-769	Sequence 769, App
26	33	100.0	106	11	US-09-864-408A-2256	Sequence 2256, Ap
27	33	100.0	106	14	US-10-004-860-769	Sequence 769, App
28	33	100.0	106	14	US-10-023-282-769	Sequence 769, App
29	33	100.0	106	16	US-10-437-963-193386	Sequence 193386, A
30	33	100.0	106	16	US-10-437-963-200270	Sequence 200270, A
31	33	100.0	111	15	US-10-425-114-42576	Sequence 42576, A
32	33	100.0	111	16	US-10-437-963-198884	Sequence 198884, A
33	33	100.0	116	16	US-10-437-963-140798	Sequence 140798, A
34	33	100.0	117	16	US-10-437-963-189086	Sequence 189086, A
35	33	100.0	118	16	US-10-437-963-165487	Sequence 165487, A
36	33	100.0	119	16	US-10-437-963-193952	Sequence 193952, A
37	33	100.0	119	15	US-10-425-114-67947	Sequence 67947, A
38	33	100.0	120	14	US-10-263-828-109	Sequence 109, App
39	33	100.0	121	16	US-10-437-963-131386	Sequence 131386, A
40	33	100.0	122	16	US-10-767-701-40561	Sequence 40561, A
41	33	100.0	124	9	US-09-925-300-1627	Sequence 1627, Ap
42	33	100.0	126	15	US-10-424-599-281122	Sequence 281122, A
43	33	100.0	135	16	US-10-437-963-130818	Sequence 130818, A
44	33	100.0	136	16	US-10-437-963-154630	Sequence 154630, A
45	33	100.0	137	9	US-09-893-737-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-10-425-114-69587
; Sequence 69587, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69587
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLB73122A03_FLI.pep
US-10-425-114-69587

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US-09-846-033B-183 (1-19) x US-10-425-114-69587 (1-239)

QY 2 TGGACGGGTGAGCGGCG 19
pb 142 TrpThrGlyGluAlaAla 147

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RESULT 2
US-10-300-616-37
; Sequence 37, Application US/10300616
; Publication No. US20030082801A1
; GENERAL INFORMATION:
; APPLICANT: BARNES, ASHLEY A.
; APPLICANT: WISE, ALAN
; APPLICANT: MARSHALL, FIONA H.
; APPLICANT: FRASER, NEIL J.
; APPLICANT: WHITE, JULIE H. M.
; APPLICANT: POORD, STEVEN M.
; TITLE OF INVENTION: NOVEL RECEPTOR
; FILE REFERENCE: PG3558US2
; CURRENT APPLICATION NUMBER: US/10/3
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: GB9819420
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Versi
; SEQ ID NO 37
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-300-616-37

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Pred. No.:	1.02e+03
Score:	33.00
Length:	15
Matches:	33.00
Conservative:	0
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Mismatches:	0
Query Match:	100.00%
Indels:	0
DB:	14
Gaps:	0

US-09-846-033B-183 (1-19) x US-10-300-616-37 (1-18)

Qy 17 CCGCCTCACCCGTCC 3
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Db 14 ProProHisProSer 18

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RESULT 3
US-09-986-480-200
; Sequence 200, Application US/09986480
; Publication No. US20030027999A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: P85001
; CURRENT APPLICATION NUMBER: US/09/986.480
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200

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; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-480-200

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Score: 33.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
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Length: 47
Matches: 5
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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US-09-846-033B-183 (1-19) x US-09-986-480-200 (1-47)

Qy 17 CCGCCTCACCCGTCC 3
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Db 10 ProProHisProSer 14

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RESULT 4
US-10-863-332-200
? Sequence 200, Application US/10863332
? Publication No. US20050064458A1
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 143 Human Secreted Proteins
? FILE REFERENCE: PS500P1
? CURRENT APPLICATION NUMBER: US/10/863,332
? PRIOR FILING DATE: 2004-06-09
? PRIOR APPLICATION NUMBER: US/09/986,480
? PRIOR FILING DATE: 2001-11-08
? PRIOR APPLICATION NUMBER: PCT/US00/12788
? PRIOR FILING DATE: 2000-05-11
? PRIOR APPLICATION NUMBER: US 60/134,068
? PRIOR FILING DATE: 1999-05-13
? NUMBER OF SEQ ID NOS: 456
? SOFTWARE: PatentIn ver. 2.0
? SEQ ID NO 200
? LENGTH: 47
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-863-332-200

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Score:	33.00	Matches:
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Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
Dg:	17	Gaps:

US-09-846-033B-183 (1-19) x US-10-863-332-200 (1-47)

Qy 17 CCGCTCACCCGTCC 3
Db 10 ProProHisProSer 14

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RESULT 5
US-09-864-761-40279
; Sequence 40279, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04

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;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 63/2,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 40279
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
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;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.4
;; OTHER INFORMATION: SWISSPROT HIT: Q13516, EVALUE 3.60e+00
;; OTHER INFORMATION: EST_HUMAN HIT: BF026119.1, EVALUE 4.50e-01
US-09-864-761-40279

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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-846-033B-183 (1-19) x US-09-864-761-40279 (1-49)

QY 17 CGGCTCACCGTCC 3
DB 25 ProProHisProSer 29

RESULT 6

US-10-424-599-152461

;; Sequence 152461, Application US/10424599

;; Publication No. US20040031072A1

;; GENERAL INFORMATION:

;; APPLICANT: La Rosa Thomas J
;; APPLICANT: Kovalic David K
;; APPLICANT: Zhou Yihua
;; APPLICANT: Cao Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 152461
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_108698C.1.pep
US-10-424-599-152461

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Pred. No.: 921 Length: 58
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-846-033B-183 (1-19) x US-10-424-599-152461 (1-58)

QY 17 CGGCTCACCGTCC 3

DB 37 ProProHisProSer 41

RESULT 7

US-10-106-698-6126

;; Sequence 6126, Application US/10106698

;; Publication No. US20030109690A1

;; GENERAL INFORMATION:

;; APPLICANT: Ruben et al.

;; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

;; FILE REFERENCE: PA00591

;; CURRENT APPLICATION NUMBER: US/10/106,698

;; CURRENT FILING DATE: 2002-03-27

;; PRIOR APPLICATION NUMBER: PCT/US00/26524

;; PRIOR FILING DATE: 2000-09-28

;; PRIOR APPLICATION NUMBER: US 60/157,137

;; PRIOR FILING DATE: 1999-09-29

;; PRIOR APPLICATION NUMBER: US 60/163,280

;; PRIOR FILING DATE: 1999-11-03

;; NUMBER OF SEQ ID NOS: 8564

;; SOFTWARE: PatentIn Ver. 3.0

;; SEQ ID NO 6126

;; LENGTH: 63

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: MISC FEATURE

;; LOCATION: (31)_

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-106-698-6126

Alignment Scores:
Pred. No.: 914 Length: 63
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-846-033B-183 (1-19) x US-10-106-698-6126 (1-63)

QY 17 CGGCTCACCGTCC 3

DB 41 ProProHisProSer 45

RESULT 8
US-10-424-599-214599
; Sequence 214599, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214599
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3580C.1.pep
US-10-424-599-214599
Alignment Scores:
Pred. No.: 912 Length: 65
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 15

US-09-846-033B-183 (1-19) x US-10-424-599-214599 (1-65)
Oy 17 CCGCCTCACCGTCC 3
Db 3 ProProHisProSer 7
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RESULT 9
US-10-437-963-180710
; Sequence 180710, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180710
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78055C.1.pep
US-10-437-963-180710
Alignment Scores:
Pred. No.: 912 Length: 65
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 16

US-09-846-033B-183 (1-19) x US-10-437-963-180710 (1-65)

Oy 17 CCGCCTCACCGTCC 3
Db 5 ProProHisProSer 9
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RESULT 10

US-10-767-701-59921
; Sequence 59921, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 59921
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(65)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: 7550665.pep
US-10-767-701-59921

Alignment Scores:
Pred. No.: 912 Length: 65
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 16

US-09-846-033B-183 (1-19) x US-10-767-701-59921 (1-65)

Oy 17 CCGCCTCACCGTCC 3
Db 61 ProProHisProSer 65
|||||

RESULT 11

US-10-424-599-201841
; Sequence 201841, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201841
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24288C.1.pep
US-10-424-599-201841
Alignment Scores:
Pred. No.: 903 Length: 72
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-846-033B-183 (1-19) x US-10-424-599-201841 (1-72)

QY 17 CCGCTCACCGCTCC 3
DB 10 ProProHisProSer 14

RESULT 12
US-10-424-599-214619
; Sequence 214619, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214619
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_35828C.1.pep
US-10-424-599-214619

Alignment Scores:
Pred. No.: 903 Length: 72
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-846-033B-183 (1-19) x US-10-424-599-214619 (1-72)

QY 17 CCGCTCACCGCTCC 3
DB 60 ProProHisProSer 64

RESULT 13
US-10-424-599-272894
; Sequence 272894, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272894
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_88446C.1.pep
US-10-424-599-272894
```

```
Alignment Scores:
Pred. No.: 903 Length: 72
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-846-033B-183 (1-19) x US-10-424-599-272894 (1-72)

QY 17 CCGCTCACCGCTCC 3
DB 41 ProProHisProSer 45

RESULT 14
US-10-437-963-162599
; Sequence 162599, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162599
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61675C.1.pep
US-10-437-963-162599

Alignment Scores:
Pred. No.: 899 Length: 76
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-846-033B-183 (1-19) x US-10-437-963-162599 (1-76)

QY 17 CCGCTCACCGCTCC 3
DB 21 ProProHisProSer 25

RESULT 15
US-10-437-963-170670
; Sequence 170670, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

```
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 170670
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68974C.1.pep
US-10-437-963-170670
```

```
Alignment Scores:
Pred. No.:      899      Length:      76
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00% Indels:      0
DB:              16      Gaps:      0
```

US-09-846-033B-183 (1-19) x US-10-437-963-170670 (1-76)

```
Oy      17 CCGCCTCACCGTCC 3
Db      60 ProProHisProSer 64
```

Search completed: April 11, 2005, 19:55:28
Job time : 77.5591 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: April 11, 2005, 18:46:20 ; Search time 18.4909 Seconds
(without alignments)
187.325 Million cell updates/sec

Title: US-09-846-033B-182
Perfect score: 29
Sequence: 1 ggagagggggcgccagtg 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566691

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/con2_1/USPTO spoal_p/US09846033/runat_11042005_185610_24081/app_query.fasta_1.796
-DB=PIR -OFT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -MODE=LOCAL
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09846033 @CGN 1 1.107 @runat_11042005_185610_24081 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
C 1	29	76.3 113 2	T28800
C 2	29	100.0 117 2	AC3421
C 3	29	100.0 166 2	S52308
C 4	29	76.3 181 2	G96715
C 5	29	76.3 182 2	C41660
C 6	29	76.3 210 2	B82522
C 7	29	100.0 234 2	T37141
C 8	29	100.0 358 2	F87315
C 9	29	100.0 388 2	AG2341
C 10	29	100.0 390 2	JC7901
C 11	29	76.3 392 2	D64493
C 12	29	100.0 422 1	JC1210
C 13	29	100.0 422 2	A55587
C 14	29	100.0 423 2	S11974

15	29	100.0	425	2	JC5850	polyketide synthas
16	29	100.0	430	2	S69228	probable polyketid
17	29	100.0	434	2	E95130	enolase [imported]
18	29	100.0	434	2	D98001	phosphopyruvate hy
C 19	29	76.3	507	2	T23959	hypothetical prote
C 20	29	76.3	519	2	C64037	hypothetical prote
C 21	29	100.0	528	2	S69589	hypothetical prote
C 22	29	76.3	673	2	T48012	hypothetical prote
C 23	29	76.3	843	1	A27340	complement C7 prec
C 24	29	76.3	899	2	H96617	probable disease r
C 25	29	100.0	2188	2	A70984	probable polyketid
C 26	28	73.7	39	2	B41933	mating pheromone E
C 27	28	73.7	76	2	AG0815	hypothetical prote
C 28	28	96.6	99	2	B38623	collagen alpha 2(I
C 29	28	73.7	133	2	I52649	circcadian protein
C 30	28	73.7	138	2	B90125	40S ribosomal prot
C 31	28	96.6	179	2	C64855	ycfj protein - Esc
C 32	28	96.6	179	2	D85674	hypothetical prote
C 33	28	96.6	179	2	H90814	hypothetical prote
C 34	28	96.6	193	2	B75493	probable molybdopt
C 35	28	73.7	207	2	H85070	hypothetical prote
C 36	28	73.7	214	2	A72326	hypothetical prote
C 37	28	96.6	220	2	A96007	hypothetical prote
C 38	28	73.7	234	2	JQ1282	hypothetical 27.3K
C 39	28	73.7	235	2	S70132	probable membrane
C 40	28	73.7	241	2	JQ1735	hypothetical 26.3K
C 41	28	96.6	241	2	E87437	ABC transporter, A
C 42	28	73.7	256	2	I36807	hypothetical prote
C 43	28	73.7	256	2	T42931	hypothetical prote
C 44	28	73.7	260	2	AG2238	hypothetical prote
C 45	28	73.7	260	2	A90330	hypothetical prote

ALIGNMENTS

RESULT 1

T28800
hypothetical protein C16E9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C:Accession: T28800
R:Geisel, C.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C16E9.
A:Reference number: Z20525
A:Accession: T28800
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-113 <GEI>
A:Cross-references: EMBL:U39677; PIDN:AAC47960.1; GSPDB:GN00028; CESP:C16E9.6
A:Experimental source: strain Bristol N2; clone C16E9
C:Genetics:
A:Gene: CESP:C16E9.6
A:Map position: X
C:Superfamily: Caenorhabditis elegans hypothetical protein C16E9.6

Alignment Scores:
Pred. No.: 592
Score: 29.00
Length: 113
Matches: 5
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Conservative: 0
Query Match: 76.32%
Mismatch: 1
Indels: 0
Gaps: 0
DB: 2

US-09-846-033B-182 (1-18) x T28800 (1-113)

QY 18 CACTCCGCCCTCTCC 1
||||| |||||
Db 88 HisCysPheProLeuser 93

RESULT 2

AC3421
hypothetical exported protein BME11353 [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3421
R;DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, S.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:1175668
A;Accession: AC3421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <CUR>
A;Cross-references: UNIPROT:Q8YQ09; GB:AE008917; PIDN:AAL52534.1; PID:g17983347; GSPDB:C
C;Genetics:
A;Experimental source: strain 16M
A;Gene: BME1133
A;Map position: 1

Alignment Scores:
Pred. No.: 589 Length: 117
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x AC3421 (1-117)

Qy 1 CGAGAGGGGGCGCAGTG 18
Db 83 GlyGluGlyAlaAlaVal 88

RESULT 3
S52308
pall protein - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52308
R;Ramos-Gonzalez, M.I.; Ramos, J.
submitted to the EMBL Data Library, July 1993
A;Reference number: S52308
A;Accession: S52308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <RAM>
A;Cross-references: UNIPROT:P43036; EMBL:X74218; NID:g861087; PIDN:CAA52294.1; PID:g6630
C;Superfamily: outer membrane protein A

Alignment Scores:
Pred. No.: 559 Length: 166
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x S52308 (1-166)

Qy 1 CGAGAGGGGGCGCAGTG 18
Db 31 GlyGluGlyAlaAlaVal 36

RESULT 4
G96715
transcription factor CRC, 87968-89174 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96715
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96715
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <STO>
A;Cross-references: UNIPROT:Q9XHD1; GB:AR005173; NID:g7705103; PIDN:AAF67782.1; GSPDB:GNI
C;Genetics:
A;Gene: F23010.23
A;Map position: 1

Alignment Scores:
Pred. No.: 552 Length: 181
Score: 29.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x G96715 (1-181)

Qy 18 CACTGCGGCCCTCTCC 1
Db 52 HisCysGlyAsnLeuSer 57

RESULT 5
C41660
vnfx protein - Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: C41660
R;Wolfinger, E.D.; Bishop, P.E.
J. Bacteriol. 173, 7565-7572, 1991
A;Title: Nucleotide sequence, and mutational analysis of the vnfENX region of Azotobacter
A;Reference number: A41660; MUID:92041669; PMID:1938952
A;Accession: C41660
A;Molecule type: DNA
A;Residues: 1-182 <WOL>
A;Cross-references: UNIPROT:O31277; GB:M74768; NID:g142407; PIDN:AAA22177.1; PID:g387572

Alignment Scores:
Pred. No.: 552 Length: 182
Score: 29.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x C41660 (1-182)

Qy 18 CACTGCGGCCCTCTCC 1
Db 139 HisCysGlyGlyLeuSer 144

RESULT 6
B82522
hypothetical protein XF2740 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82522
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <SIM>

A:Cross-references: UNIPROT:Q9P9Y0; GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF8552
 A:Experimental source: strain 9a5C
 R:Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Gensbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2740

Alignment Scores:
 Pred. No.: 540 Length: 210
 Score: 29.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 66.67% Mismatches: 0
 Query Match: 76.32% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x B82522 (1-210)

QY 18 CACTCGGGCCCTCTCC 1

Db 150 TyrCysGlyProLeuAla 155

RESULT 7

T37141

probable membrane protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T37141

R:Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A:Reference number: Z21622

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T37141

A:Molecule type: DNA

A:Residues: 1-234 <HAR>

A:Cross-references: UNIPROT:Q9S1R5; EMBL:AL109972; PIDN:CA853266.1; GSPDB:GN00070; SCOE

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOE:SCJ9A.05c

Alignment Scores:
 Pred. No.: 532 Length: 234
 Score: 29.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x T37141 (1-234)

QY 1 GGAGAGGGGGCCGCGAGTG 18

Db 169 GlyGluGlyAlaAlaVal 174

RESULT 8

F87315

SIS domain protein [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: F87315

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: F87315

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STO>

A:Cross-references: UNIPROT:Q9AAR1; GB:AE005673; NID:gl3421722; PIDN:AAK22522.1; GSPDB:

C:Genetics:

A:Gene: CC0535

Alignment Scores:

Pred. No.: 500 Length: 358
 Score: 29.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x F87315 (1-358)

QY 1 GGAGAGGGGGCCGCGAGTG 18

Db 29 GlyGluGlyAlaAlaVal 34

RESULT 9

AG2341

3-oxoacyl-[acyl-carrier-protein] synthase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AG2341

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2341

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <KUR>

A:Cross-references: UNIPROT:Q8YPB2; GB:BA000019; PIDN:BA875985.1; PID:gl17133421; GSPDB:

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all4286

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Alignment Scores:

Pred. No.: 494 Length: 388
 Score: 29.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x AG2341 (1-388)

QY 1 GGAGAGGGGGCCGCGAGTG 18

Db 210 GlyGluGlyAlaAlaVal 215

RESULT 10

JC7901

inwardly-rectifying ATP-sensitive potassium channel Kir6.2, pore -forming subunit - Bul

C:Species: Rana catesbeiana (bullfrog)

C>Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004

C:Accession: JC7901

R:Park, P.J.; Chung, J.Y.; Byun, H.G.; Seog, D.H.; Kim, S.K.

Biosci. Biotechnol. Biochem. 66, 2279-2282, 2002

A:Title: Molecular cloning of a pore-forming subunit (Kir6.2 gene) of the ATP-sensitive

A:Reference number: JC7901; MUID:22333953; PMID:12450150

A:Accession: JC7901

A:Molecule type: mRNA
A:Residues: 1-390 <PAR>
A/Cross-references: UNIPROT:Q7LZ07; GB:AF454384
A/Experimental source: liver
C/Comment: This protein, which forms the potassium ion-selective pore, is involved in di-
lateral excitability, smooth muscle relaxation, neurotransmitter release, and brain ische-
mia.
C/Genetics:
A/Gene: Rckir6.2
C/Keywords: transmembrane protein

Alignment Scores:
Pred. No.: 493 Length: 390
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x JC7901 (1-390)

Qy 1 GGAGAGGGCGCGCAGTG 18
Db 103 GlyGluglyAlaAlaVal 108

RESULT 11
D64493
non-specific lipid-transfer protein homolog - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: D64493
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
J.; Raich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: D64493
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-392 <BUL>
A/Cross-references: UNIPROT:Q58944; GB:U67595; GB:L77117; NID:g1592170; PIDN:AAB99567.1;
C/Genetics:
A/Map position: FOR1526429-1527607

Alignment Scores:
Pred. No.: 493 Length: 392
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x D64493 (1-392)

Qy 18 CACTGGCGCCCTCTCC 1
Db 205 HisCysSerProValSer 210

RESULT 12
JC1210
polyketide beta-ketoacyl synthase (EC 2.3.1.-) chain 1 - Streptomyces cyaneus
N/Alternate names: beta-ketoacyl synthase; curA protein
C/Species: Streptomyces cyaneus
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: JC1210; C33073
R/Berg, S.; Uhlen, M.
Gene 117, 131-136, 1992
A/Title: Analysis of a polyketide synthesis-encoding gene cluster of Streptomyces curaco
A/Reference number: JC1210; MUID:92354925; PMID:1644304
A/Accession: JC1210
A/Molecule type: DNA
A/Residues: 1-422 <BER>

A:Molecule type: mRNA
A:Residues: 1-422 <PAR>
A/Cross-references: UNIPROT:Q02578; GB:X62518; NID:g45888; PIDN:CAA44380.1; PID:g581629
A/Note: the source is designated as Streptomyces curaco
C/Genetics:
A/Gene: curA
A/Start codon: GTG
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
C/Keywords: acyltransferase
P;23-414/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Alignment Scores:
Pred. No.: 488 Length: 422
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-846-033B-182 (1-18) x JC1210 (1-422)

Qy 1 GGAGAGGGCGCGCAGTG 18
Db 238 GlyGluglyAlaAlaVal 243

RESULT 13
A55587
ketosynthase - Streptomyces griseus
C/Species: Streptomyces griseus
C/Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
C/Accession: A55587
R/Yu, T.W.; Bibb, M.J.; Revill, W.P.; Hopwood, D.A.
J. Bacteriol. 176, 2627-2634, 1994
A/Title: Cloning, sequencing, and analysis of the griseusin polyketide synthase gene clu
A/Reference number: A55587; MUID:94222841; PMID:8169211
A/Accession: A55587
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-422 <YUA>
A/Cross-references: UNIPROT:Q54217; GB:X77865; NID:g488770; PIDN:CAA54858.1; PID:g581665
C/Genetics:
A/Start codon: GTG
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
P;23-414/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Alignment Scores:
Pred. No.: 488 Length: 422
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x A55587 (1-422)

Qy 1 GGAGAGGGCGCGCAGTG 18
Db 238 GlyGluglyAlaAlaVal 243

RESULT 14
S11974
polyketide beta-ketoacyl synthase alpha - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S11974; T35611
R/Davis, N.K.; Chater, K.F.
Mol. Microbiol. 4, 1679-1691, 1990
A/Title: Spore colour in Streptomyces coelicolor A3(2) involves the developmentally regu
A/Reference number: S11972; MUID:91171868; PMID:2077356
A/Accession: S11974
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-423 <DAV>
A/Cross-references: UNIPROT:P23155; EMBL:X55942; NID:g46919; PIDN:CAA39408.1; PID:g46922
R/Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999
A:Reference number: Z21584
A:Accession: T35611
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-423 <SEE>
A:Cross-references: EMBL:AL079356; PIDN:CAB45606.1; GSPDB:GN00070; SCOEDB:SC6G9.15
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC6G9.15
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein]
F:24-415/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Alignment Scores:
Pred. No.: 488 Length: 423
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x S11974 (1-423)

QY 1 GGAGAGGGCGCGCAGTG 18
DB 239 GlyGluGlyAlaAlaVal 244

RESULT 15
JC5850
polyketide synthase (EC 2.-.-.-) chain 1 - Actinomadura hibisca
C:Species: Actinomadura hibisca
C:Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5850
R:Dairi, T.; Hamano, Y.; Igarashi, Y.; Furumai, T.; Oki, T.
Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997
A:Title: Cloning and nucleotide sequence of the putative polyketide synthase genes for P
A:Reference number: JC5850; MUID:97480928; PMID:9339544
A:Accession: JC5850
A:Molecule type: DNA
A:Residues: 1-425 <DAI>
A:Cross-references: UNIPROT:O32451; DDBJ:D87924
C:Comment: This enzyme catalyzes repeated condensation cycles of acyl-CoA, affecting the
C:Genetics:
A:Gene: pms1
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein]
C:Keywords: transferase
F:30-421/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Alignment Scores:
Pred. No.: 487 Length: 425
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-182 (1-18) x JC5850 (1-425)

QY 1 GGAGAGGGCGCGCAGTG 18
DB 245 GlyGluGlyAlaAlaVal 250

Search completed: April 11, 2005, 19:11:43
Job time : 20.4509 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:45:50 ; Search time 85.7455 Seconds
(without alignments)
214.995 Million cell updates/sec

Title: US-09-846-033b-182
Perfect score: 29
Sequence: 1 ggagagggggccgcagtg 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224100

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09846033/runat_11042005_185609_24068/app.query.fasta_1.796
-DB=Uniprot -QFMT=fasta -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09846033@cgn 1 1 427 @runat_11042005_185609_24068 -NCPUs=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
Description					

No matches found

Search completed: April 11, 2005, 19:09:42
Job time : 85.7455 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:41:45 ; Search time 107.091 Seconds
(without alignments)
137.238 Million cell updates/sec

Title: US-09-846-033B-183
Perfect score: 35
Sequence: 1 atggacgggtgagcgcg 19

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p model -DEV=xlp
-Q=/cgn2_1/USPTC spool_p/US09846033/runat_11042005.185608.24062/app_query.fasta_1.796
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09846033 @CEN 1 1 475 @runat 11042005.185608.24062 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	398	ABU11688	Abu11688 Human MDD
2	35	100.0	656	Adg22363	Adg22363 Cyanophag
3	35	100.0	776	Aau31431	Aau31431 Novel hum
C 4	33	100.0	9	Aar83816	Aar83816 SH3-bindi
C 5	33	100.0	15	Aar62600	Aar62600 Cryoglobu
C 6	33	100.0	47	Aab56106	Aab56106 Human sec
C 7	33	100.0	49	Aam20312	Aam20312 Peptide #
C 8	33	100.0	49	Abb40780	Abb40780 Peptide #
C 9	33	100.0	49	Aam34546	Aam34546 Peptide #
C 10	33	100.0	49	Abb24981	Abb24981 Protein #

C 11	33	100.0	49	4	AAM74432	Human bon
C 12	33	100.0	49	4	AAM61640	Human bra
C 13	33	100.0	49	4	ABG56226	Human liv
C 14	33	100.0	49	5	ABG44324	Human pap
C 15	33	100.0	53	4	AAO08643	Human pol
C 16	33	100.0	57	5	ABP10302	Human ORF
C 17	33	100.0	63	4	AAU66460	Human col
C 18	33	100.0	64	4	AAU66460	Propionib
C 19	33	100.0	64	6	ABM62979	Propionib
C 20	33	100.0	68	4	AAU23699	Human EST
C 21	33	100.0	68	4	ABG14140	Novel hum
C 22	33	100.0	79	5	ABP08619	Human ORF
C 23	33	100.0	79	5	ABP35471	Human ORF
C 24	33	100.0	81	3	AAU16021	Arabidops
C 25	33	100.0	82	5	ADK35812	Novel hum
C 26	33	100.0	83	3	AAU44882	Zea mays
C 27	33	100.0	83	4	AAU24347	Human EST
C 28	33	100.0	88	4	AAU59472	Human sec
C 29	33	100.0	88	6	ABU19711	Human sec
C 30	33	100.0	88	6	ABP99716	Human sec
C 31	33	100.0	88	6	ABR01197	Human gen
C 32	33	100.0	88	6	ADA98310	Human sec
C 33	33	100.0	88	7	ADC20478	Human sec
C 34	33	100.0	91	5	ABP43047	Human ova
C 35	33	100.0	92	5	AAU47908	Human zin
C 36	33	100.0	98	6	ABR41575	Human DIT
C 37	33	100.0	99	4	AAO06553	Human pol
C 38	33	100.0	101	4	AAU32704	Novel hum
C 39	33	100.0	104	3	AAU54147	Human pan
C 40	33	100.0	106	2	AAW88840	Polypepti
C 41	33	100.0	106	4	ABB50816	Human syn
C 42	33	100.0	106	5	ABP32155	Human syn
C 43	33	100.0	106	6	ABO45073	Novel hum
C 44	33	100.0	106	7	ABO26553	Protein a
C 45	33	100.0	111	3	AAU16020	Arabidops

ALIGNMENTS

RESULT 1
ABU11688
ID ABU11688 standard; protein; 398 AA.
XX
AC ABU11688;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human MDDT polypeptide SEQ ID 635.
XX

MDDT; human; disease detection and treatment molecule polypeptide;
anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
gene therapy; protein replacement therapy; cell proliferative disorder;
cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;
anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
psoriasis; hepatitis.

OS Homo sapiens.

XX
XX WO200279449-A2.
XX
XX 10-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-US009944.
XX
XX 28-MAR-2001; 2001US-0279619P.
XX
XX 29-MAR-2001; 2001US-0280067P.
XX
XX 29-MAR-2001; 2001US-0280068P.
XX
XX 16-MAY-2001; 2001US-0291280P.
XX
XX 17-MAY-2001; 2001US-0291829P.
XX
XX 17-MAY-2001; 2001US-0291849P.
XX
XX 19-JUN-2001; 2001US-0299428P.

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PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstein EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34678.
XX
XX New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
XX Claim 27; SEQ ID NO 635; 339pp + Sequence Listing; English.
XX
XX This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDPT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipariatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDP polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 398 AA;
Alignment Scores:
Pred. No.: 238 Length: 398
Score: 35.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-846-033B-183 (1-19) x ABU11688 (1-398)
Qy 2 TGGACGGGTGAGCGGCG 19
Db 122 TrpThrGlyGluAlaAla 127
RESULT 2
ADG22363
ID ADG22363 standard; protein; 656 AA.
XX
XX ADG22363;
AC ADG22363;
XX
DT 26-FEB-2004 (first entry)
XX
DE Cyanophages S-2L encoded protein #108.
XX
XX genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
XX
XX Cyanophage S-2L.
XX
XX FR2839079-A1.
XX
XX 31-OCT-2003.
XX
PF 30-APR-2002; 2002FR-00005424.
XX
DR 30-APR-2002; 2002FR-00005424.
XX
PA (INSP) INST PASTEUR.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PA (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
XX
PI Marliere P, Kaminski PA, Galisson F, Bouzon M, Pochet S;
PI Weissbach J, Saurin W, Robert C, Vico V;
XX
DR WPI; 2004-045746/05.
DR N-PSDB; ADG22255.
XX
XX New genomic sequence for cyanophage S-2L, useful for identifying genes
PT for synthesis of 2,6-diaminopurine bases or polynucleotides containing
PT them.
XX
XX Claim 6; SEQ ID NO 109; 423pp; French.
XX
XX The invention relates to the entire genome of cyanophage S-2L, and to the
CC protein encoded by it. Genes isolated from the genome of S-2L are useful
CC for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine),
CC particularly D, dTMP and dTTP, or polynucleotides containing these bases,
CC polymerases involved in metabolism of D-bases and deoxynucleotide
CC analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides,
CC can be used for detection and/or identification of S-2L, and for
CC identifying agents that modulate synthesis of D-bases or polynucleotides
CC containing them, and fusions of S-2L polypeptides with an antigen can be
CC used to raise specific antibodies, useful for detecting S-2L. This
CC sequence corresponds to one of the proteins encoded by the cyanophage S-
CC 2L genome.
XX
SQ Sequence 656 AA;
Alignment Scores:
Pred. No.: 236 Length: 656
Score: 35.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-846-033B-183 (1-19) x ADG22363 (1-656)
Qy 2 TGGACGGGTGAGCGGCG 19
Db 289 TrpThrGlyGluAlaAla 294
RESULT 3
AAU31431
ID AAU31431 standard; protein; 776 AA.
XX
XX AAU31431;
AC AAU31431;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1922.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX
XX 26-JAN-2001; 2001US-00770160.
XX
```

XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
XX Claim 20; Page 437; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 776 AA;

Alignment Scores:
Pred. No.: 236 Length: 776
Score: 35.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x AAU31431 (1-776)

QY 2 TGGACGGGTGACGGCGC 19
DB 98 TrpThrGlyGluAlaAla 103

RESULT 4
AAR83816
ID AAR83816 standard; peptide; 9 AA.
XX AAR83816;
XX
DT 14-FEB-1996 (first entry)
XX
XX SH3-binding proline-rich p47(phox) analogue #3.
DE
KW p47(phox); p67(phox); NADPH oxidase complex; proline-rich region; PTPase;
KW SH3 domain; inhibition; dynamin; cytochrome b245; reperfusion injury;
KW septic shock; arthritis; asthma; vinculin; inflammatory bowel disease;
KW adult respiratory distress syndrome; ischaemic heart disease.
XX
OS Synthetic.
XX
XX GB2285047-A.
PN
XX 28-JUN-1995.
PD
XX
PF 07-DEC-1994; 94GB-00024674.
XX
XX 21-DEC-1993; 93GB-00026083.
PR
XX 07-JAN-1994; 94GB-00000248.
XX
XX (YAMA) YAMANOUCHI UK LTD.
PS

PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Finan PM, Gout IT, Kellie S, Shimizu Y, Waterfield MD;
XX WPI; 1995-217703/29.
XX
XX New polypeptide(s) with antiinflammatory action - inhibit NADPH oxidase
PT system.
XX
XX Claim 2; Page 8; 17pp; English.
XX
XX The protein p47(phox) (AAR83825) interacts with protein p67(phox) in the
CC NADPH oxidase complex via a C-terminal proline-rich region of p47(phox)
CC binding to at least one C-terminal SH3 domain of p67(phox). The peptides
CC AAR83814-24 were derived from the proline-rich region of p47(phox) and
CC show inhibitory activity towards the binding of p47(phox) to p67(phox) as
CC compared to the proline-rich region of a range of other proteins
CC (AAR83826-30). The inhibitory peptides can be used for the treatment of
CC chronic or acute inflammatory diseases e.g. septic shock, arthritis,
CC asthma, adult respiratory distress syndrome, ischaemic heart disease,
CC reperfusion injury or inflammatory bowel disease
XX
SQ Sequence 9 AA;

Alignment Scores:
Pred. No.: 8.52e+07 Length: 9
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-846-033B-183 (1-19) x AAR83816 (1-9)

QY 17 CGCCTCACCGCTCC 3
DB 5 ProProHisProSer 9

RESULT 5
AAR62600
ID AAR62600 standard; peptide; 15 AA.
XX
XX AAR62600;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1995 (first entry)
XX
XX Cryoglobulinemia type II diagnostic reagent and immunogen.
DE
XX Cryoglobulinemia type II; human hepatitis C; HCV; immunogen;
KW specific diagnostic reagent; vaccine.
XX
XX Synthetic.
XX
XX WO9426886-A2.
PN
XX 24-NOV-1994.
PD
XX 05-MAY-1994; 94WO-IT0000054.
PF
XX 11-MAY-1993; 93IT-RM000301.
PR
XX (RICE-) IST RICERCH BIOL MOLECOLARE ANGELETTI.
PA
XX Felici F, Luzzago A, Nicosia A, Monaci P, Cortese R;
XX WPI; 1995-006783/01.
XX
XX Selecting immunogens and diagnostic reagents using phage libraries -
PT expressing oligopeptide(s) on the surface, useful for vaccines, partic.
PT against hepatitis virus and auto-immune disease.
XX
XX Claim 11; Page 55; 79pp; English.
PS

XX AAR62596-R62600 and AAR63867-R63873 are specific diagnostic reagents and
 CC immunogens for type II cryoglobulinemia caused by/or associated with
 CC human hepatitis C virus (HCV). These peptides mimic the HCV surface
 CC antigen (HCAg), therefore when injected into individuals not immune to
 CC HCV they elicit an immune response, specifically the production of anti-
 CC HCAg antibodies. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX SQ Sequence 15 AA;
 CC
 Alignment Scores:
 Pred. No.: 629 Length: 15
 Score: 33.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-846-033B-183 (1-19) x AAR62600 (1-15)
 QY 17 CCGCTCACCCGTCC 3
 Db 8 ProProHisProSer 12
 RESULT 6
 AAB56106
 ID AAB56106 standard; protein; 47 AA.
 AC AAB56106;
 XX
 XX 13-MAR-2001 (first entry)
 DT
 DE Human secreted protein sequence encoded by gene 30 SEQ ID NO:200.
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; gene therapy; pathological condition;
 KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
 KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; skin aging; food additive; preservative.
 XX OS Homo sapiens.
 XX WO200070042-A1.
 PN
 XX 23-NOV-2000.
 PD
 XX 11-MAY-2000; 2000WO-US012788.
 PF
 XX 13-MAY-1999; 99US-0134068P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
 PI Duan RD, Florence KA, Soppet DR;
 FI
 XX WPI; 2000-679828/66.
 DR N-PSDB; AAC99847.
 XX
 XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PS Claim 11; Page 957; 1065pp; English.
 XX
 XX The polynucleotide sequences given in AAC99818 to AAC99977 encode the
 CC human secreted proteins given in AAB56077 to AAB56362. Human secreted
 CC proteins have activities based on the tissues and cells the genes are
 CC expressed in. Examples of activities include: immunosuppressive;

CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
 CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
 CC virucide; fungicide; and ophthalmological. The human secreted
 CC polynucleotides and proteins can be used to prevent, treat or ameliorate
 CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. They are also used in diagnosing a pathological
 CC condition or susceptibility to a pathological condition. Disorders which
 CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. The proteins can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The proteins can also be used as a
 CC food additive or preservative to increase or decrease storage
 CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
 CC in the exemplification of the present invention
 XX SQ Sequence 47 AA;

Alignment Scores:
 Pred. No.: 617 Length: 47
 Score: 33.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-846-033B-183 (1-19) x AAB56106 (1-47)

QY 17 CCGCTCACCCGTCC 3
 Db 10 ProProHisProSer 14

RESULT 7

ID AAM20312 standard; protein; 49 AA.

AC AAM20312;

DT 12-OCT-2001 (first entry)

DE Peptide #6746 encoded by probe for measuring cervical gene expression.

KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

OS Homo sapiens.

PN WO200157278-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US0000670.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

PS Claim 27; SEQ ID NO 25138; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 49 AA;

Alignment Scores: 617 Length: 49
Pred. No.: 33.00 Matches: 5
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 4

US-09-846-033B-183 (1-19) x AAM20312 (1-49)

OY 17 CCGCCTACCCGTC 3
DB 25 ProProHisProSer 29

RESULT 8

ABB40780
ID ABB40780 standard; peptide; 49 AA.

XX ABB40780;

XX 04-FEB-2002 (first entry)

XX Peptide #8286 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX

PS Claim 27; SEQ ID NO 33415; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 49 AA;

Alignment Scores: 617 Length: 49
Pred. No.: 33.00 Matches: 5
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 4

US-09-846-033B-183 (1-19) x ABB40780 (1-49)

OY 17 CCGCCTACCCGTC 3

DB 25 ProProHisProSer 29

RESULT 9

AAM34546

ID AAM34546 standard; protein; 49 AA.

XX AAM34546;

XX 17-OCT-2001 (first entry)

XX Peptide #8583 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 34815; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders

XX SQ Sequence 49 AA;

Alignment Scores: 617 Length: 49

Pred. No.: 33.00

Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x AAM34546 (1-49)

QY 17 CCGCCTCACCGTCC 3
DB 25 ProProHisProSer 29

RESULT 10

ABB24981
ID ABB24981 standard; protein; 49 AA.

XX AC ABB24981;

DT 23-JAN-2002 (first entry)

DE Protein #6980 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

XX OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US0000666.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-488899/53.

XX PT Single exon nucleic acid probes for analyzing gene expression in human hearts.
XX PS Claim 15; SEQ ID NO 26751; 530pp; English.

XX CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease.

XX CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 49 AA;

Alignment Scores:
Pred. No.: 617 Length: 49
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x ABB24981 (1-49)

QY 17 CCGCCTCACCGTCC 3
DB 25 ProProHisProSer 29

RESULT 11

AAM74432
ID AAM74432 standard; protein; 49 AA.

XX AC AAM74432;

XX DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34738.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US0000668.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PS WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

XX PS Example 4; SEQ ID NO 34738; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention

XX SQ Sequence 49 AA;

Alignment Scores:
Pred. No.: 617 Length: 49
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x AAM74432 (1-49)

QY 17 CCGCCTCACCGTCC 3

DB 25 ProProHisProSer 29

RESULT 12

```
AAM61640
ID AAM61640 standard; protein; 49 AA.
XX
AC AAM61640;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33745.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 33745; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 49 AA;

Alignment Scores:
Pred. No.: 617 Length: 49
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x AAM61640 (1-49)

QY 17 CGCCTCACCGCTCC 3
DB 25 ProProHisProSer 29

RESULT 13
ABG56226
ID ABG56226 standard; peptide; 49 AA.
XX
AC ABG56226;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 34874.
XX

Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 34874; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: the sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from Wipo at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 49 AA;

Alignment Scores:
Pred. No.: 617 Length: 49
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x ABG56226 (1-49)

QY 17 CGCCTCACCGCTCC 3
DB 25 ProProHisProSer 29

RESULT 14
ABG44324
ID ABG44324 standard; peptide; 49 AA.
XX
AC ABG44324;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33989.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
```

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX Homo sapiens.
XX WO200186003-A2.
XX 15-NOV-2001.
XX 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX Claim 27; SEQ ID NO 33989; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 49 AA;
XX Alignment Scores:
XX Pred. No.: 617 Length: 49
XX Score: 33.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 5 Gaps: 0
XX US-09-846-033B-183 (1-19) x ABC44324 (1-49)
XX QY 17 CCGCCTCACCCGTC 3
XX DB 25 ProProHisProSer 29
XX RESULT 15
XX AAO08643
XX ID AAO08643 standard; protein; 53 AA.
XX AC AAO08643;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 22535.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PP 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX N-PSDB; AAI88574.
XX DR WPI; 2001-514838/56.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 22535; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO3910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 53 AA;
XX Alignment Scores:
XX Pred. No.: 616 Length: 53

Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-183 (1-19) x AAO08643 (1-53)

Qy 17 CCGCCTCACCGTCC 3

Db 14 ProProHisProSer 18

Search completed: April 11, 2005, 19:00:53
Job time : 109.091 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 19:09:59 ; Search time 71.3455 Seconds
(without alignments)
167.522 Million cell updates/sec

Title: US-09-846-033B-182
Perfect score: 29
Sequence: 1 ggagaggggcgccgagtg 18

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 2834941

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID Description

No matches found

Search completed: April 11, 2005, 19:55:26
Job time : 71.5955 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 11, 2005, 18:49:31 ; Search time 21.1091 Seconds
(without alignments)
127.308 Million cell updates/sec

Title: US-09-846-033B-182
Perfect score: 29
Sequence: 1 ggagagggggccgcagtg 18

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1026956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITIS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US09846033@cgn 1 1.107 @runat_11042005_185610_24092 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	29	76.3	91	3	US-08-851-843A-220
C 3	29	76.3	91	3	US-08-974-549A-339
C 4	29	76.3	91	3	US-08-854-050-220
C 5	29	76.3	91	3	US-09-430-323-220
C 6	29	76.3	91	4	US-09-402-181B-339
C 7	29	76.3	91	4	US-09-721-456-339
C 8	29	100.0	115	5	PCT-US95-13658-2
C 9	29	76.3	132	4	US-09-270-767-34541
C 10	29	76.3	132	4	US-09-270-767-49758
C 11	29	76.3	214	3	US-08-861-774E-66
C 12	29	100.0	250	4	US-09-252-991A-30155

C 13	29	76.3	254	4	US-09-134-000C-4740	Sequence 4740, Ap
C 14	29	100.0	311	3	US-08-961-083-184	Sequence 184, App
C 15	29	100.0	311	4	US-09-536-784-184	Sequence 184, App
C 16	29	100.0	313	4	US-09-949-016-10072	Sequence 10072, A
C 17	29	100.0	332	4	US-09-270-767-43137	Sequence 43137, A
C 18	29	100.0	401	4	US-09-902-540-11439	Sequence 11439, A
C 19	29	100.0	407	4	US-09-107-433-4986	Sequence 4986, Ap
C 20	29	100.0	420	3	US-08-847-065-19	Sequence 19, Appl
C 21	29	100.0	420	4	US-09-829-382-19	Sequence 19, Appl
C 22	29	100.0	430	2	US-08-809-740A-2	Sequence 2, Appl
C 23	29	100.0	434	4	US-09-583-110-3817	Sequence 3817, Ap
C 24	29	76.3	440	4	US-09-252-991A-24173	Sequence 24173, A
C 25	29	100.0	459	3	US-08-977-001-1	Sequence 1, Appl
C 26	29	76.3	901	4	US-09-538-092-826	Sequence 826, App
C 27	29	100.0	1046	4	US-09-252-991A-30284	Sequence 30284, A
C 28	29	76.3	1213	4	US-09-543-681A-6478	Sequence 6478, Ap
C 29	28	73.7	15	2	US-08-553-257A-54	Sequence 54, Appl
C 30	28	73.7	15	2	US-08-553-257A-56	Sequence 56, Appl
C 31	28	73.7	15	4	US-09-441-992-56	Sequence 54, Appl
C 32	28	73.7	15	4	US-09-441-992-56	Sequence 56, Appl
C 33	28	73.7	18	4	US-10-158-847-133	Sequence 133, Appl
C 34	28	73.7	26	4	US-10-158-847-37	Sequence 37, Appl
C 35	28	96.6	65	4	US-09-252-991A-23443	Sequence 23443, A
C 36	28	73.7	70	4	US-09-270-767-61351	Sequence 61351, A
C 37	28	73.7	71	4	US-09-673-395A-251	Sequence 251, App
C 38	28	96.6	85	4	US-09-632-287A-12	Sequence 12, Appl
C 39	28	96.6	100	2	US-08-963-601-2	Sequence 2, Appl
C 40	28	96.6	100	4	US-08-735-848-2	Sequence 2, Appl
C 41	28	73.7	111	4	US-09-087-031E-9	Sequence 9, Appl
C 42	28	73.7	111	4	US-09-087-031E-14	Sequence 14, Appl
C 43	28	73.7	111	4	US-09-087-031E-16	Sequence 16, Appl
C 44	28	73.7	112	4	US-09-087-031E-17	Sequence 17, Appl
C 45	28	96.6	129	4	US-09-481-620A-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-12004
; Sequence 12004, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12004

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12004

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Pred. No.: 1.1e+03
Score: 29.00
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Best Local Similarity: 66.67%
Query Match: 76.32%
DB: 4
Matches: 69
Conservative: 4
Mismatches: 1
Indels: 0
Gaps: 0

US-09-846-033B-182 (1-18) x US-09-489-039A-12004 (1-69)

Qy 18 CACTGCGGCCCTCTCC 1

Db 49 HisCysSerProLeuThr 54

RESULT 2

US-08-851-843A-220

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; Sequence 220, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6093809a1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-220

Alignment Scores:
Pred. No.: 1.08e+03 Length: 91
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-182 (1-18) x US-08-851-843A-220 (1-91)
Qy 18 CACTGCGGCCCTCTCC 1
Db 60 HisCysSerProLeuAla 65

RESULT 3
US-08-974-549A-339
; Sequence 339, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
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; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-339
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Score: 29.00 Matches: 4
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Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-182 (1-18) x US-08-974-549A-339 (1-91)

QY 18 CACTGCGGCCCTCTCC 1
DB 60 HisCysSerProLeuAla 65

RESULT 4
US-08-854-050-220
; Sequence 220 Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-854-050-220

Alignment Scores: 91
Pred. No.: 1.08e+03 Length: 4
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-182 (1-18) x US-08-854-050-220 (1-91)

QY 18 CACTGCGGCCCTCTCC 1
DB 60 HisCysSerProLeuAla 65

RESULT 5
US-09-430-323-220
; Sequence 220 Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 220:

US-09-430-323-220

Alignment Scores: Length: 91
Pred. No.: 1.08e+03 Matches: 4
Score: 29.00 Conservative: 1
Percent Similarity: 83.33% Mismatches: 1
Best Local Similarity: 66.67% Indels: 0
Query Match: 76.32% Gaps: 0
DB: 3

US-09-846-033B-182 (1-18) x US-09-430-323-220 (1-91)

Qy 18 CACTGGCGCCCTCTCC 1
Db 60 HisCysSerProLeuAla 65

RESULT 6

US-09-402-181B-339
; Sequence 339, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Auserhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 339:

SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
US-09-402-181B-339

Alignment Scores: Length: 91
Pred. No.: 1.08e+03 Matches: 4
Score: 29.00 Conservative: 1
Percent Similarity: 83.33% Mismatches: 1
Best Local Similarity: 66.67% Indels: 0
Query Match: 76.32% Gaps: 0
DB: 4

US-09-846-033B-182 (1-18) x US-09-402-181B-339 (1-91)

Qy 18 CACTGGCGCCCTCTCC 1
Db 60 HisCysSerProLeuAla 65

RESULT 7

US-09-721-456-339
; Sequence 339, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 339:
US-09-721-456-339

Alignment Scores:
Pred. No.: 1.08e+03 Length: 91
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-721-456-339 (1-91)

QY 18 CACTGGCGCCCTCTCC 1
Db 60 HisCysSerProLeuAla 65

RESULT 8
PCT-US95-13658-2
; Sequence 2, Application PC/TUS9513658
; GENERAL INFORMATION:
; APPLICANT: Sverlow, Genadie G.
; APPLICANT: Halverson, Joy L.
; TITLE OF INVENTION: Identification and Isolation of Flea
; TITLE OF INVENTION: Allergens
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94114187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13658
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A60359/BTR;ZOOG2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 7811989
; TELEFAX: (415) 3983249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
PCT-US95-13658-2

Alignment Scores:
Pred. No.: 1.06e+03 Length: 115
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-846-033B-182 (1-18) x PCT-US95-13658-2 (1-115)

QY 1 GGAGAGGGCGCGCAGTG 18
Db 45 GlyGluGlyAlaAlaVal 50

RESULT 9
US-09-270-767-34541
; Sequence 34541, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34541
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34541

Alignment Scores:
Pred. No.: 1.05e+03 Length: 132
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-270-767-34541 (1-132)

QY 18 CACTGGCGCCCTCTCC 1
Db 30 HisCysAsnProLeuAsn 35

RESULT 10
US-09-270-767-49758
; Sequence 49758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49758
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49758

Alignment Scores:
Pred. No.: 1.05e+03 Length: 132

Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-270-767-49758 (1-132)

Qy 18 CACTGGGCCCCCTCTCC 1
Db 30 HisCysAsnProLeuAsn 35

RESULT 11

US-08-861-774E-66
; Sequence 66, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; TITLE OF INVENTION: BIOACTIVE MOLECULES
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 66
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Siphula certities
US-08-861-774E-66

Alignment Scores:
Pred. No.: 1.02e+03 Length: 214
Score: 29.00 Matches: 5
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-182 (1-18) x US-08-861-774E-66 (1-214)

Qy 18 CACTGGGCCCCCTCTCC 1
Db 60 HisCysGlyArgLeuSer 65

RESULT 12

US-09-252-991A-30155
; Sequence 30155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30155
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30155

Alignment Scores:
Pred. No.: 1.01e+03 Length: 250
Score: 29.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-252-991A-30155 (1-250)

Qy 1 GGAGAGGGGGCGCAGTG 18
Db 72 GlycylGlyAlaAlaVal 77

RESULT 13

US-09-134-000C-4740
; Sequence 4740, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6912
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4740
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4740

Alignment Scores:
Pred. No.: 1.01e+03 Length: 254
Score: 29.00 Matches: 4
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 1
Query Match: 76.32% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-134-000C-4740 (1-254)

Qy 18 CACTGGGCCCCCTCTCC 1
Db 212 HisCysAlaProLeuAla 217

RESULT 14

US-08-961-083-184
; Sequence 184, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-184

Alignment Scores:
Pred. No.: 998 Length: 311
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-846-033B-182 (1-18) x US-08-961-083-184 (1-311)

QY 1 GGAGAGGGGGCGCAGTG 18
Db 140 GlyGluGlyAlaAlaVal 145

RESULT 15

US-09-536-784-184
Sequence 184, Application US/09536784
Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-536-784-184

Alignment Scores:
Pred. No.: 998 Length: 311
Score: 29.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-846-033B-182 (1-18) x US-09-536-784-184 (1-311)

QY 1 GGAGAGGGGGCGCAGTG 18
Db 140 GlyGluGlyAlaAlaVal 145

Search completed: April 11, 2005, 19:13:58
Job time : 23.1091 secs

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